

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

Run on: March 12, 2004, 10:11:55 ; Search time 3735 Seconds
(without alignments)

10061.154 Million cell updates/sec

Title: US-09-821-831-3

Perfect score: 86/
Sequence: 1 acagctcgcgcgcgcaagcag...ccgcgcacaccgacaac 867

Scoring table: IDENTITY_NUC

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database

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- 1: gb.ba.*
- 2: gb.hg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.cv.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
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- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
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- 19: em.mu.*
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- 40: em.hgo.mus.*
- 41: em.hgo.other.*

Pred. No. is the number of results predicted by chance to have a

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2	866	99.9	3259	10	RNNGFR
3	746.6	86.1	3441	10	BC038385
4	656.6	75.7	1321	10	AF105282
5	629.2	72.6	1600	6	AA3530
6	629.2	72.6	1600	6	AR098123
7	629.2	72.6	3386	6	AR153575
8	629.2	72.6	3386	6	AX658249
9	629.2	72.6	3386	6	AX741452
10	629.2	72.6	3386	6	AX771496
11	629.2	72.6	3386	6	HUMANFR
12	629.2	72.6	3425	9	BC050309
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14	362.6	41.8	241243	2	AC094206
15	338.2	39.0	217904	2	AC015915
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17	276.4	31.9	62885	2	AC126343
18	276.4	31.9	147775	9	AC015656
19	276.4	31.9	163344	2	AC060233
20	276.4	31.9	186617	9	AC006487
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45	45.8	5.3	1391	6	AR156431

ALIGNMENTS

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AX827823		
LOCUS		
AX827823	3259 bp	DNA linear PAT 12-DEC-2003

DEFINITION	Sequence 55 / from patent EP1344037
ACCESSION	AX827823
VERSION	AX827823.1 GI:39838011

SOURCE ORGANISM	Pathogen	Host	Incubation Period	Signs and Symptoms	Diagnosis	Treatment	Prevention
Rattus norvegicus (Norway rat)	Leishmania infantum	Human	2-6 months	Maculopapular rash, fever, weight loss	PCR, serology	Antimonial drugs	Vector control, avoid bites
Rattus norvegicus	Leishmania infantum	Dog	2-6 months	Maculopapular rash, fever, weight loss	PCR, serology	Antimonial drugs	Vector control, avoid bites

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE AUTHORS TITLE	
Boess, F., Suter-Dick, L. and Wolf, D. Methods for the toxicity prediction of a compound	

JOURNAL Patent: EP 1344834-A 557 17-SEP-2003;

F. HOFFMANN-LA ROCHE AG (CH)

FEATURES

source

Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:10116"

ORIGIN

Query Match 99.9%; Score 866; DB 6; Length 3259;

Best Local Similarity 100.0%; Pred. No. 3.1e-175;

Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 301 CCGTGTGGAACCCCGGCGGCGGCGGCTGGAATGTTTACATCTCCGAGTGTGAGCGCCACTGAGC 360
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RESULT 2

RNNGFR

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

RNNGFR 3259 bp mRNA linear ROD 21-MAR-1995
Rat mRNA for fast nerve growth factor receptor (NGFR).
X05137
X05137.1 GI:56755
nerve growth factor receptor.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
Rattus.
1 (bases 1 to 3259)
Radeke, M.J., Misko, T.P., Heu, C., Herzberg, J.A. and Shooter, E.M.
Gene transfer and molecular cloning of the rat nerve growth factor
receptor.
Nature 325 (6105), 593-597 (1987)
87115859
3027580
PUBMED
MEDLINE
JOURNAL
TITLE
AUTHORS
REFERENCE
1 (bases 1 to 3259)
Radeke, M.J., Misko, T.P., Heu, C., Herzberg, J.A. and Shooter, E.M.
Gene transfer and molecular cloning of the rat nerve growth factor
receptor.
Nature 325 (6105), 593-597 (1987)
87115859
3027580
PUBMED
MEDLINE
JOURNAL
TITLE
AUTHORS
REFERENCE

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CDS

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ORIGIN

Query Match 99.9%; Score 866; DB 10; Length 3259;

Best Local Similarity 100.0%; Pred. No. 3.1e-175;

Matches 866; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 CAGCTCCGGGCGGCGGCGGCTGAGACCGCATGGCAGTTTACAGTTCAGCCGACGACCATC 61
DB 1 CAGCTCCGGGCGGCGGCGGCTGAGACCGCATGGCAGTTTACAGTTCAGCCGACGACCATC 60
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DB 61 GGTGCGGAGGCGGCGGCGGCTAGAGAGGCGGCGGCTGAGCGGCGGAGGCGTGCATGAGGA 120
QY 122 GGGGAGGCTGCTGCTGCGAGCGGCATGACCGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTG 181
DB 121 GGGGAGGCTGCTGCTGCGAGCGGCATGACCGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTG 180
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Qy      422 CAGACGATGACGTGTGACAGATGTGTCTATGTCTCTACGACGACGACGACGACGAC 481
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Qy      602 ACCCGTGTCTACCTGTGACGCGTGTGTGCGAGGACACTGTGACGCGCACTTACGCGAC 661
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RESULT 3
BC038365          3441 bp  mRNA      linear  ROD 21-OCT-2003
LOCUS           Mus musculus nerve growth factor receptor (TNFR superfamily, member
DEFINITION     16), mRNA (cDNA clone MGC:35588 IMAGE:5367638), complete cds.
ACCESSION      BC038365
VERSION        BC038365.1  GI:23468246
KEYWORDS       Mus musculus (house mouse)
SOURCE         MGC.
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclerognathi; Muride; Murinae; Mus.
1 (bases 1 to 3441)
Strusberg,R.L., Fengold,E.A., Grouse,L.H., Derge,J.G.,
Carrinci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
Altschul,S.F., Collins,F.S., Wagner,L., Sherman,C.M., Schuler,G.D.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Ditschenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schaefer,T.E., Brownstein,M.J., Uesdin,T.B., Toshiyuki,S.,
Carrinci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahy,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shcherch,A.,
Boutard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalek,U., Smalins,D.E.,

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TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL

REMARK COMMENT

Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 3441)

Strusberg,R.
 Direct Submission
 Submitted (01-OCT-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-rt@mail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louieged, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
 Series: IRAP Plate: 53 Row: 1 Column: 13
 This clone was selected for full length sequencing because it
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 Location/Qualifiers

FEATURES source

gene

CDS

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 present in a variety of proteins with apoptotic functions.
 Some (but not all) of these domains form homotypic and

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 QY 591 CAACCAAGTGAACCGGCTTACCTGACAGGTGTGAGAGACACTAGAGCCAGTTACG 650
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 QY 651 CGAGTGCACGCGCTGTGGCTGTATGTGAATGCAAGATCCCTGTGATGATCCCAAG 710
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 QY 711 GTCTACGCGCGCGAGGCTCCGACAGACAGCGCCAGACCCAGAGAGCTGAGTTCC 770
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RESULT 5

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 DEFINITION Sequence 1 from Patent WO9506723.
 A43530
 VERSION A43530.1 GI:2298718
 KEYWORDS

SOURCE unidentified
 ORGANISM unidentified.

REFERENCE 1 (bases 1 to 1600)
 Bordignon, C. and Mavillio, F.
 AUTHORS METHOD OF MARKING EUKARYOTIC CELLS BY THE USE OF A CELL SURFACE
 TITLE RECEPTOR AS A MARKER
 JOURNAL Patent: WO 9506723-A 1 09-MAR-1995;
 BOEHRINGER MANNHEIM GMBH (DE)
 COMMENT Other publication IT 1261947 960603
 Other publication CA 2170757 950309.
 FEATURES
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ORIGIN

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 QY 506 TGGGCTGCGGACTCGTGTCTCTGCTCCAGACAAACAGACACAGTGTGTGAAGATGCC 565
 Db 502 CGGGCTCGGGCTCGTGTCTCTGCTCCAGGACAAACAGACACAGTGTGTGAAGATGCC 561
 QY 566 CAGAGGCAATCTACAGACAGAGCCACACAGTGTGACCCGTGCTTACCTTGCACAGTGT 625
 Db 562 CGGACGCGACATTAATCCGACGAGCGCAACACAGTGTGACCCGTGCTTGCACAGTGT 621
 QY 626 GCGAGGACACTGAGCGCAGTTACGCGAGTGCACGCGCTGAGCTGATGTGATGCGAG 685
 Db 622 GCGAGGACACTGAGCGCAGTTACGCGAGTGCACACGCTGAGCTGAGCGCGAGGAGG 681
 QY 686 AGATCCCTGTGTGATGATCCCAAGTGTACGCGCGCGAGGCTTCCAGACACACAGCCG 745
 Db 682 AGATCCCTGTGTGATGATCCCAAGTGTACGCGCGCGAGGCTTCCAGACACACAGCCG 741
 QY 746 CAGACACCCAGAGACCTGAGTGTCTCCAGACAGACAGACCTTGTACCACTGATGAGTGCAG 805
 Db 742 CAGACACCCAGAGACCTGAGTGTCTCCAGACAGACAGACCTTGTACCACTGATGAGTGCAG 801
 QY 806 ATATGTGACCACTGTGATGAGGCGAGTCCAGCCTGTGTGACCCGCGGACCAACCGACA 865
 Db 802 GTGTGTGACCACTGTGATGAGGCGAGTCCAGCCTGTGTGACCCGCGGACCAACCGACA 861
 QY 866 AC 867
 Db 862 AC 863

RESULT 6

AR098123 1600 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 1 from patent US 6074836.
 AR098123
 VERSION AR098123.1 GI:12807380
 KEYWORDS

SOURCE Unknown.

REFERENCE 1 (bases 1 to 1600)
 Bordignon, C. and Mavillio, F.

AUTHORS Method of marking eukaryotic cells
 TITLE Patent: US 6074836-A 1 13-JUN-2000;
 JOURNAL
 FEATURES Location/Qualifiers

source 1..1600

/organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 72.6%; Score 629.2; DB 6; Length 1600;
 Best Local Similarity 85.0%; Pred. No. 1,7e-124;
 Matches 716; Conservative 0; Mismatches 123; Indels 3; Gaps 1;
 QY 26 GGAAGGCATCGAGTTCAGCTCAGGCGACCAATCGGCTCCGAGCGGACTGAGCTAG 85
 Db 25 GGGGGGCGCTGAGAGCGCAGCGACCGACCCCACTAGTCCGCAAAAGCGACCGAGCTGG 84
 QY 86 AAGCGAGAGCGCTGACGCGCGAGGCGCTGCAATGAGAGAGGCGAGGTGCTGCTGACGCGCCA 145

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2004, 16:27:22 ; Search time 21 seconds
(without alignments)
1149.718 Million cell updates/sec

Title: US-09-821-831-4

Sequence: 1 MRRAGACSMDBRLRLILL.....MTTVNGSSQPVYRTGTDN 251

Scoring table: BIOSUM62
Gapex 10.0, Gapext 0.5

Searched: 28366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 28366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1387	100.0	425	1 A26431	nerve growth facto
2	1344	89.7	427	1 GQHUN	nerve growth facto
3	883.5	63.7	416	1 JN0006	nerve growth facto
4	215.5	15.5	461	1 GQRTT1	tumor necrosis fac
5	214	15.4	277	2 I37552	OX40 homolog - hum
6	202	14.6	305	2 A46476	B cell-associated
7	202	14.6	454	1 GQMT1	tumor necrosis fac
8	197.5	14.2	455	1 GQHUT1	tumor necrosis fac
9	196.5	14.2	325	2 B43692	T2 protein - rabbi
10	193.5	14.0	326	1 GQVZML	OX40 antigen precu
11	189.5	13.7	271	2 SI2783	gene OX40 protein
12	186.5	13.4	272	2 I48700	gene murine tumor
13	182.5	13.2	474	2 B38634	tumor necrosis fac
14	180.5	13.0	474	2 B38634	death receptor-6 -
15	178	12.8	651	2 UC7705	B-cell activation
16	175.5	12.7	277	2 A60771	tumor necrosis fac
17	175	12.6	435	2 I54182	laminin alpha-1 ch
18	171.5	12.4	3075	2 SI4458	tumor necrosis fac
19	171	12.3	461	1 UC4302	tumor necrosis fac
20	170.5	12.3	461	1 A35356	Fas antigen precu
21	163	11.8	324	2 UC3395	membrane glycoprot
22	161.5	11.6	493	2 UC3486	Fas soluble protei
23	159.5	11.5	314	2 I37383	variant-specific s
24	158	11.4	557	2 A48434	apoptosis-mediatin
25	156	11.2	335	2 A40036	apoptosis-mediatin
26	154.5	11.1	327	2 A46484	laminin alpha-4 ch
27	154	11.1	1816	1 S68960	trophozoite surfac
28	151.5	10.9	667	2 A48579	serine protease
29	151.5	10.9	1548	2 S34583	

30	148	10.7	255	2 I38426	lymphocyte activat
31	143.5	10.3	677	2 C42125	trophozoite cystei
32	142.5	10.3	3712	2 S18253	laminin alpha-1 ch
33	142	10.2	1274	2 T42017	cysteine rich prot
34	141	10.2	348	2 T28623	hypothetical prote
35	141	10.2	349	2 D36858	gene G4R protein -
36	139	10.0	349	2 T10053	G2R protein - vari
37	139	10.0	3635	2 T10053	laminin alpha 5 ch
38	137.5	9.9	1372	2 T25933	hypothetical prote
39	137	9.9	3084	1 MMSA	laminin alpha-1 ch
40	136.5	9.8	260	1 A46517	CD27 antigen precu
41	136.5	9.8	1187	2 T18355	hypothetical prote
42	136	9.8	962	2 UC5871	subtilisin-like pr
43	136	9.8	975	2 UC5570	subtilisin-like pr
44	134.5	9.7	354	2 T22274	hypothetical prote
45	134.5	9.7	3707	2 S18252	heparan sulfate pr

ALIGNMENTS

RESULT 1
A26431
nerve growth factor receptor precursor, low affinity - rat
N/Alternate names: NGF receptor
C/Species: Rattus norvegicus (Norway rat)
C/Date: 10-Sep-1999 #sequence #revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: A26431; PH1229
R/Adeske, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A/Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A/Reference number: A26431; PMID:87115859; PMID:3027580
A/Accession: A26431
A/Molecule type: mRNA
A/Residues: 1-425 <RAD>
A/Cross-references: GB:X05137; MID:956755; PIDN:CA28783.1; PID:956756
R/Metels, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A/Title: Regulatory elements and transcriptional regulation by testosterone and retinoic
A/Reference number: PH1229; PMID:93077038; PMID:1446821
A/Accession: PH1229
A/Molecule type: DNA
A/Residues: 1-20 <MET>
A/Cross-references: GB:X61265
C/Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C/Comment: The cysteine-rich region of the extracellular domain may form part or all of
C/Comment: this protein is thought to form a high-affinity receptor when it associates w
C/Genetics:
A/Intons: 20/3
C/Supersfamily: nerve growth factor receptor; NGF receptor repeat homology
C/Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F.1.29/Domain: signal sequence #status predicted <SI>
F.30-251/Product: nerve growth factor receptor #status predicted <EXT>
F.30-251/Domain: extracellular #status predicted <EXT>
F.33-66/Domain: NGF receptor repeat homology <NG1>
F.68-109/Domain: NGF receptor repeat homology <NG2>
F.110-148/Domain: NGF receptor repeat homology <NG3>
F.150-190/Domain: NGF receptor repeat homology <NG4>
F.198-249/Region: serine/threonine-rich
F.252-273/Domain: transmembrane #status predicted <MEM>
F.274-425/Domain: intracellular #status predicted <INT>
F.61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 1387; DB 1; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.5e-90; Mismatches 0; Indels 0; Gaps 0;
Matches 251; Conservative 0;

Cy 1 MRRAGACSMDBRLRLILLIGVSSGAKETSTGTYTHSGCCACNLGSGVAPCGA 60
Db 1 MRRAGACSMDBRLRLILLIGVSSGAKETSTGTYTHSGCCACNLGSGVAPCGA 60
Cy 61 NOTVCEPCLDNVTFSDVSAATEPCKPTECLGTSNSAPCEVDEADVAICACAYYODEET 120

Db 61 NOTVEPCLDNTFSDVSAATEPCKPCTECLGLQSMNAPCVAEDADVACRACVYQDEET 120
 QY 121 GHCEACVCEVSGGLVFSQCDKQNTVCECECEEGTYSDEANHVDPCLPTVCEDTERQLE 180
 Db 121 GHCEACVCEVSGGLVFSQCDKQNTVCECECEEGTYSDEANHVDPCLPTVCEDTERQLE 180
 QY 181 CTNPADACEEIPGRMIPRSTPEGSSTAPSTQCEPVPPEODLVSTVADMTVMGSS 240
 Db 181 CTNPADACEEIPGRMIPRSTPEGSSTAPSTQCEPVPPEODLVSTVADMTVMGSS 240
 QY 241 QPVVTRGTTDN 251
 Db 241 QPVVTRGTTDN 251

RESULT 2
 GORUN
 nerve growth factor receptor precursor, low affinity [validated] - human
 N/Alternate names: NGF receptor
 C/Species: Homo sapiens (man)
 C/Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text_change 08-Dec-2000
 C/Accession: A25218; A60204; S21689; I57638
 R/Johnson, D.; Lanthan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.
 Cell 47, 545-554, 1986
 A/Title: Expression and structure of the human NGF receptor.
 A/Reference number: A25218; PMID:87051725; PMID:3022937
 A/Accession: A25218
 A/Molecule type: mRNA
 A/Residues: 1-427 <JOH>
 A/Cross-references: GB:M4764; NID:G189204; PIDN:AA59544.1; PID:G189205
 R/Marano, N.; Dietzschold, B.; Farley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, P.;
 J. Neurochem. 48, 225-232, 1987
 A/Title: Purification and amino terminal sequencing of human melanoma nerve growth factor
 A/Reference number: A60204; PMID:87065574; PMID:3025363
 A/Accession: A60204
 A/Molecule type: protein
 A/Residues: 29-31, 'T', '33-42', 'TT', '45-46', 'TX', '50-51', 'XX', '54-56' <MAR>
 A/Experimental source: melanoma cell line A875
 A/Note: This sequence has been corrected by a note added in proof to follow the nucleoti
 R/Vissavajjala, P.; Leszyk, J.D.; Lin-Goske, J.; Ross, A.H.
 Arch. Biochem. Biophys. 294, 244-252, 1992
 A/Title: Structural domains of the extracellular domain of human nerve growth factor rec
 A/Reference number: S21689; PMID:92198017; PMID:1372492
 A/Accession: S21689
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 183-208 <VIS>
 R/Sehgal, A.; Patil, N.; Chao, M.
 Mol. Cell. Biol. 8, 3160-3167, 1988
 A/Title: A constitutive promoter directs expression of the nerve growth factor receptor
 A/Reference number: I57638; PMID:89096903; PMID:12850461
 A/Accession: I57638
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-22 <RES>
 A/Cross-references: GB:M21621; NID:G189206; PIDN:AA36363.1; PID:G189207
 C/Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
 C/Comment: The cysteine-rich region of the extracellular domain may form part or all of
 C/Comment: This protein is thought to form a high-affinity receptor when it associates w
 C/Comment: This receptor undergoes both N- and O-linked glycosylation.
 C/Genetics:
 A/Genes: GDB:NGFR
 A/Cross-references: GDB:120214; OMTM:162010
 A/Map position: 17q21.1-17q22
 C/Superfamily: nerve growth factor receptor; NGF receptor repeat homology
 C/Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
 F:1-29/Dominant: signal sequence #status predicted <SIG>
 F:29-427/Product: nerve growth factor receptor #status experimental <MAT>
 F:29-250/Dominant: extracellular #status predicted <EXT>
 F:32-65/Dominant: NGF receptor repeat homology <NG1>
 F:67-108/Dominant: NGF receptor repeat homology <NG2>
 F:109-147/Dominant: NGF receptor repeat homology <NG3>
 F:149-189/Dominant: NGF receptor repeat homology <NG4>

F:197-248/Region: serine/threonine-rich
 F:251-272/Dominant: transmembrane #status predicted <TM>
 F:273-427/Dominant: intracellular #status predicted <INT>
 F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.7%; Score 1244; DB 1; Length 427;
 Best Local Similarity 90.7%; Pred. No. 6, 4e-80;
 Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 4 AGAAGSAMRLLILLIIGVSGGAKETCSGLITHSECCCKACNLGGVAPGGANOT 63
 Db 3 AGATGRAMDPRILLILLIGVSLGAKKAPGLYTHSECCCKACNLGGVAPGGANOT 62
 QY 64 VCEPCLDNTFSDVSAATEPCKPCTECLGLQSMNAPCVAEDADVACRACVYQDEET 123
 Db 63 VCEPCLDNTFSDVSAATEPCKPCTECLGLQSMNAPCVAEDADVACRACVYQDEET 122
 QY 124 EACVCEVSGGLVFSQCDKQNTVCECECEEGTYSDEANHVDPCLPTVCEDTERQLE 183
 Db 123 EACVCEVSGGLVFSQCDKQNTVCECECEEGTYSDEANHVDPCLPTVCEDTERQLE 182
 QY 184 WADACEEIPGRMIPRSTPEGSSTAPSTQCEPVPPEODLVSTVADMTVMGSSQPV 243
 Db 183 WADACEEIPGRMIPRSTPEGSSTAPSTQCEPVPPEODLVSTVADMTVMGSSQPV 242
 QY 244 VTRGTTDN 251
 Db 243 VTRGTTDN 250

RESULT 3
 UN0006
 nerve growth factor receptor, low affinity precursor - chicken
 N/Alternate names: NGF receptor
 C/Species: Gallus gallus (chicken)
 C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: JN0006; A60504
 R/Larage, T.H.; Weckamp, G.; Heider, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reic
 Neuron 2, 1123-1134, 1989
 A/Title: Structure and developmental expression of the nerve growth factor receptor in t
 A/Reference number: JN0006; PMID:9016579; PMID:2630385
 A/Accession: JN0006
 A/Molecule type: mRNA
 A/Residues: 1-416 <LAR>
 A/Experimental source: embryonic chick brain
 R/Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
 Dev. Biol. 137, 287-304, 1990
 A/Title: Structure and developmental expression of the chicken NGF receptor.
 A/Reference number: A60504; PMID:90152140; PMID:2154393
 A/Accession: A60504
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 21-35, 'Y', '37-172', 'K', '174-275', 'S', '277-395', 'R', '397-416' <HEU>
 C/Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
 C/Comment: The cysteine-rich region of the extracellular domain may form part or all of
 C/Comment: This protein is thought to form a high-affinity receptor when it associates v
 C/Superfamily: nerve growth factor receptor; NGF receptor repeat homology
 C/Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
 F:1-20/Dominant: signal sequence #status predicted <SIG>
 F:21-416/Product: nerve growth factor receptor #status predicted <MAT>
 F:21-239/Dominant: extracellular #status predicted <EXT>
 F:24-57/Dominant: NGF receptor repeat homology <NG1>
 F:59-100/Dominant: NGF receptor repeat homology <NG2>
 F:101-139/Dominant: NGF receptor repeat homology <NG3>
 F:141-181/Dominant: NGF receptor repeat homology <NG4>
 F:189-237/Region: serine/threonine-rich
 F:240-261/Dominant: transmembrane #status predicted <TM>
 F:262-416/Dominant: intracellular #status predicted <INT>
 F:52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.7%; Score 883.5; DB 1; Length 416;
 Best Local Similarity 66.1%; Pred. No. 9, 7e-55;
 Matches 156; Conservative 33; Mismatches 44; Indels 3; Gaps 1;

QY 266 GCGAAGCGCTGGCCCAAGCCCTCCGAGACCAACCAACCTGTGTGAACCTGGCTGAGACA 325
 Db 262 GCGAGGGGTGGCCCAAGCCCTGTGTGAGACCAACCAACCTGTGTGAGCCCTGTGAGACA 321
 QY 326 ATGTTCATTTCTCCGATGTGTGAGCCCACTGAGCCGTCAAGCCGTGACCCGAGTGGC 385
 Db 322 GCGTGAAGTTCTCCGATGTGTGAGCCCACTGAGCCGTCAAGCCGTGACCCGAGTGGC 381
 QY 386 TGGGCTTCGAGAGCATGTCCGCTCTCTGTGTGAGAGGACGATGCAAGTGTGAGATGTG 445
 Db 382 TGGGCTTCGAGAGCATGTCCGCTCTCTGTGTGAGAGGACGATGCAAGTGTGAGATGTG 441
 QY 446 CCTATGGCTACTACAG 505
 Db 442 CCTATGGCTACTACAG 501
 QY 506 TGGGCTTCGAGAGCATGTCTCTCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 565
 Db 502 GCGGCTTCGAGAGCATGTCTCTCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 561
 QY 566 CAGAGGGGACATCTACAG 625
 Db 562 CCGAGGGGACATCTACAG 621
 QY 626 GCGAGGACACTGAG 685
 Db 622 GCGAGGACACTGAG 681
 QY 686 AGATTCCTCTGTGTGATGTGATGATGATGATGATGATGATGATGATGATGATGATG 745
 Db 682 AGATTCCTCTGTGTGATGTGATGATGATGATGATGATGATGATGATGATGATGATG 741
 QY 746 CCAGACCCAG 805
 Db 742 CCAGACCCAG 801
 QY 806 ATATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 865
 Db 802 GTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 861
 QY 866 AC 867
 Db 862 AC 863
 RESULT 5
 AA23423
 ID AA23423 standard; DNA; 3386 BP.
 XX AA23423;
 DT 19-JAN-2000 (first entry)
 XX
 DE Human neutrophin receptor p75NTR DNA.
 XX
 KW Propagatoric; dependence domain; p75NTR; androgen receptor; DCC;
 KW huntingtin polypeptide; Machado-Joseph disease; SCAL; SC2; SC6;
 KW atrophin-1; cell death; apoptosis; Huntington's disease; head trauma;
 KW Alzheimer's disease; Kennedy's disease; spinocerebellar ataxia; stroke;
 KW dentatorubropallidolysian atrophy; cell proliferation; cell survival;
 KW neoplastic; malignant; autoimmune; fibrotic; ss.
 XX
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 FH 114..1197
 FT CDS /tag= a
 FT /product= "p75NTR"
 XX
 PN MO9945944-A1.
 XX
 PD 16-SBP-1999.

XX 11-MAR-1999; 99WO-US005250.
 PF 12-MAR-1998; 98US-00041886.
 XX (BURN-) BURNHAM INST.
 PA Bredesen DE, Radzideh S;
 DR WPI: 1999-561617/47.
 XX P-PSDB; AA733483.
 XX
 PT New propagatoric dependence peptides, used to develop products for
 PS treating, e.g. Alzheimer's disease.
 XX Disclosure; Page 80-82; 1999P; English.
 CC This invention describes novel pure propagatoric dependence peptides
 CC which comprise a sequence of an active dependence domain selected from
 CC dependence polypeptides consisting of p75NTR, androgen receptor, DCC
 CC huntingtin polypeptide, Machado-Joseph disease gene product, SCAL, SC2,
 CC SC6 and atrophin-1 polypeptide. The propagatoric peptides are capable of
 CC inducing cell death and can be used to develop products to mediate or
 CC inhibit apoptosis. The methods can be used for reducing the severity of a
 CC propagatoric dependence domain mediated pathological conditions e.g.
 CC Huntington's disease, Alzheimer's disease, Kennedy's disease,
 CC spinocerebellar ataxia, dentatorubropallidolysian atrophy, Machado-
 CC Joseph disease, stroke or head trauma. They can also be used for reducing
 CC the severity of a pathological condition mediated by upregulated cell
 CC proliferation or cell survival e.g. neoplastic, malignant, autoimmune or
 CC fibrotic conditions. This sequence encodes the human p75NTR neurotrophin
 CC receptor described in the method of the invention
 XX
 SQ Sequence 3386 BP; 656 A; 1104 C; 1030 G; 596 T; 0 U; 0 Other;
 Query Match 72.6%; Score 629.2; DB 2; Length 3386;
 Best Local Similarity 85.0%; Pred. No. 4e-153;
 Matches 716; Conservative 0; Mismatches 123; Indels 3; Gaps 1;
 QY 26 GAGAGCGATGCGATTCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 85
 Db 25 GAGAGCGATGCGATTCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 84
 QY 86 AAGCGAGCGCTGAG 145
 Db 85 AAGCGAGCGCTGAG 141
 QY 146 TGGACCGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 205
 Db 142 TGGACCGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 201
 QY 206 AGACATGTTCCACAG 265
 Db 202 AGACATGTTCCACAG 261
 QY 266 GCGAAGCGCTGGCCCAAGCCCTCCGAGACCAACCAACCTGTGTGAACCTGGCTGAGACA 325
 Db 262 GCGAAGCGCTGGCCCAAGCCCTCCGAGACCAACCAACCTGTGTGAACCTGGCTGAGACA 321
 QY 326 ATGTTCATTTCTCCGATGTGTGAGCCCACTGAGCCGTCAAGCCGTGACCCGAGTGGC 385
 Db 322 GCGTGAAGTTCTCCGATGTGTGAGCCCACTGAGCCGTCAAGCCGTGACCCGAGTGGC 381
 QY 386 TGGGCTTCGAGAGCATGTCCGCTCTCTGTGTGAGAGGACGATGCAAGTGTGAGATGTG 445
 Db 382 TGGGCTTCGAGAGCATGTCCGCTCTCTGTGTGAGAGGACGATGCAAGTGTGAGATGTG 441
 QY 446 CCTATGGCTACTACAG 505
 Db 442 CCTATGGCTACTACAG 501
 QY 506 TGGGCTTCGAGAGCATGTCTCTCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 565

RESULT 6	
AB235044	
ID	AB235044 standard; cDNA; 3386 BP.
XX	
AC	AB235044;
XX	
DT	05-FEB-2003 (first entry)
XX	
DE	Human gene expression profile polynucleotide SEQ ID NO 156.
XX	
XX	Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
KM	bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
KW	tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
KW	gene expression; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200274979-A2.
XX	
PD	26-SEP-2002.
XX	
PF	20-MAR-2002; 2002MO-US008456.
XX	
PR	20-MAR-2001; 2001US-0276947P.
XX	
PA	(ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX	
PI	Wan J, Wang Y;
XX	
DR	WPI; 2002-740862/80.
XX	
PT	New gene expression profile generated from primary, endothelial,
PT	epithelial, and muscle cell types, useful for identifying disease
PT	pathologies involving alterations of gene expression, e.g. cancer.
XX	
PS	Claim 3; Page 380-381, 850pp; English.
XX	
CC	The invention relates to a gene expression profile comprising one or more
CC	Genes (AB234889-AB235692) and generated from a cell type. The cell type
CC	is a coronary artery endothelium, umbilical artery or vein endothelium,
CC	aortic endothelium, dermal microvascular endothelium, pulmonary artery
CC	endothelium, myometrium microvascular endothelium, keratinocyte
CC	epithelium, bronchial epithelium, mammary epithelium, prostate
CC	epithelium, renal cortical epithelium, renal proximal tubule epithelium,
CC	small airway epithelium, renal epithelium, umbilical artery smooth
CC	muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,

742 CCAGCACCAGGAGCCTGAGGCACCTCCAGACACAGACCTCATAGCCAGCACGGTGCAG 801


```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: one-off(1512)
; OTHER INFORMATION: /function= "Sati cleavage site"
US-08-602-791-1
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Query Match	72.6%;	Score 629.2;	DB 3;	Length 1600;
Best Local Similarity	85.0%;	Pred. No. 2.9e-152;		
Matches 746; Conservative	0;	Mismatches 123;	Indels 3;	Gaps 1

QY	26	GGAGCCCATGCAAGTTCACCTCAGCGACACCAATCGGTCTGCGAGACCGAATGACTG	85
Db	25	GGGGGGGGCGCTGGAGGCGCAAGCGACAGGCCCAATGATCCGCAAAACGGACCGAAGCTGG	84
QY	86	AAGCGAGCGCTGACCGCCCGAGGCGCTGCATGAGAGAGGAGCGAGTCTGCTGCAGGCCCA	145
Db	85	AAATTCAGAGCGCTCCCGCGGAGAGCGAGGCG--GATGGGGGCAAGGTGCCACCGGCGGCA	141
QY	146	TGAGACGGAGTGCAGCTGCTGCTGCTGCATTTCAAGAGTGTCTCTCGAGAGTGCACAG	205
Db	142	TGAGACGGAGCGGGCGCTGCTGCTGCTGTGTGCTTCTGGGGGTGTCCCTTGGAGGTGCCAAG	201
QY	206	AGCAATGTTCCACAGGCTCTGTACACCCACAGCGAGAGTGTGTGAAGCTTGCAACTTGG	265
Db	202	AGCAATGCCCAAGAGGCTGTGTACACACAGGGGTGTGTGTGCAAAAGCTTGCAACTTGG	261
QY	266	GGCAAGCGCTGAGCCCAAGCCCTCGAGAGCCACAGACCGTGTGTGACCCCTGCTTGACA	325
Db	262	GGAGAGGTGTGGCCCGCTTGTGTGAGCCACAGACCGTGTGTGACCCCTGCTTGACA	321
QY	326	ATGTTCATTTCTCCGATGTGTGTGAGAGGCACTGAGCGGTGCAGACCGTGTGACCGAATGGC	385
Db	322	GGGTGAGCTTCTCCGACGTGTGTGAGGCGACCGAGCCGTGTGAACCTGTGACCGAATGGC	381
QY	386	TGGGCTCTGCAAGACATGTCCGCTCCCTGTGTGTGAGGCAAGCATGTGTCAGATGTG	445
Db	382	TGGGCTCTCAGAGCAATGTGCGCGCTGTGTGTGAGGCGACAGCGCTGTGTGCGCTGGG	441
QY	446	CGATGAGCTATPACACAGACAGAGAGACATGGCCACTGTGAGAGCTTGGACGCTGTGCGAG	505
Db	442	CGTACGCTATPACACAGATGAGACGATGGGCGCTGTGAGAGCTTGGACGCTGTGCGAG	501
QY	506	TGGGCTCTGAGACTCGTGTCTCTCTGCGAGACAAACAGACACATGTGTGAAGATGCC	565
Db	502	CGGCTCTGGGCGCTCGTGTCTCTCTCAGAGACAGACAAACACGTTGTGCAAGATGGC	561
QY	566	CAGAGGCAATCTCAGACAGAGCAACCAAGTGAACCCCTGTCCTACCTGCAAGCGTGT	625
Db	562	CGAGCGGCAATCTCAGACAGAGGCAACCAAGTGAACCGGTGCTCTCCTGCAAGCGTGT	621
QY	626	GCGAGGACACTAGGCCCGCACTTACCGAGATGACCGCCCTGGGCTGTAGTCTGAATTCGAAG	685
Db	622	GCGAGGACACTAGGCGCCAGCTCCGCGAGTGAACCGTGGGCTCGAAGCGCGAGTGTGAGG	681
QY	686	AGATCCCTGTGCATGATGCCAAGGTATCGCCGCCCGAGAGGCTTCGACAGGACAGCGC	745
Db	682	AGATCCCTGTGCATGATTTACCGAGTGCACCCCGAGAGGCTTCGACAGGACAGCGC	741
QY	746	CGAGACCCGAGAGGCGCTGTGAGTTCCTCCAGACCAAGACCTTGTATCCAGTACAGTGTGG	805
Db	742	CGAGACCCGAGAGGCGCTGTGAGACCTCCAGACCAAGACCTTATAGCAAGCACGAGTGGAG	801
QY	806	ATATGTGACCACTGTGATGGGCAAGTCCGACCGTGTATGTGATCCCGGCGGACCAAGGACA	865
Db	802	GTTGGTGTACCAAGTGTATGGGCAAGTCCAGCCCGTGTGTATGCCAGGACCAAGGACGACA	861
QY	866	AC 867	
Db	862	AC 863	

Sequence 1, Application US/09/041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Eredeesen, Dale E.
APPLICANT: Radlacen, Shariot
TITLE OF INVENTION: Propeptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3386 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 114..1395
US-09-041-886-1

Query Match	72.6%	Score 629.21	DB 3	Length 3366
Best Local Similarity	85.0%	Prod. No. 3,5e-152		
Matches	716	Conservative 0	Mismatches 123	Indels 3
				Gaps 1
Qy	26	GGAGCGCATCGCAGTTCAAGTCCAGCGCAGCAGCATCGGTCTGCGAGCGGAACTGAGCTAG	85	
Dp	25	GGGGGGCGGTGAGCGCAGCGCAGCAGCCCATCAGTCCGAAAGCGGACCGAGCTGG	84	
Qy	86	AAGCGGAGCGCGTGAAGACCGCGGAGCGCTGCATATGAGAGAGGCGAGGTGCTGCTCAGCGCA	145	
Dp	85	AATCTAGAGGCTCGCCGCGGAGGCGGCGC---GATGGGAGCAGGTGCTCACCAGCGCCTGCGCA	141	
Qy	146	TGGACCGAGCTGCGCTGCTGTGTGTGTAATTTAGAGGGTGTCTTCTGAGGTGCCAAG	205	
Dp	142	TGAGCGGCGCGCGCTGTGCTGTGTGTGCTTCTGCGGGGTGTCCCTTGGAGGTGCCAAG	201	
Qy	206	AAGACATGTTCACACAGGCGCTGTACACCAACGCGGAGAGTGTCCAAAGCTCAACTTGG	265	
Dp	202	AGGCATGCCCAACAGGCGCTGTACACCAACAGCGGTAGTGTCCAAAGCTCAACTTGG	261	
Qy	266	GCGAAGCGCTGGCGCCAGCCCTTGCAGGACCAACGACCGTGTGTGAACCTTCCCTGAGACA	325	
Dp	262	GCGAGGAGTGTGCTCCAGCTTGTGTGAGACCAACAGACCGTGTGTGAGCCCTTCCCTGAGACA	321	
Qy	326	ATATTTCATTTCCTCCATGTGTGTGAGCGCACACTAGCGCTCAAGCGGTACACCGAGTACC	385	
Dp	322	GCGTACGTTCTTCCCAACCGTGTGAGCGCGACCAAGCGGTGTCAAGCGGTCAACCGAGTGG	381	
Qy	386	TGGGCTTGACAGCATGTTCGCTCCCTGTGTGTGAGGACAGCATGCAAGTGTGCAATGTG	445	

Query Match	100.0%;	Score 867;	DB 9;	Length 867
Best Local Similarity	100.0%;	Pred. No. 4.2e-237;		

```

Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGCTCCGGCGGGGAGAGGCGCTGGAGCCGATGCGAGTTCAAGCTCAGCCGAGACCAT 60
Db 1 ACAGCTCCGGCGGGGAGAGGCGCTGGAGCCGATGCGAGTTCAAGCTCAGCCGAGACCAT 60
QY 61 CGGTCTGCGGAGCGGAGCTAGAGTAAAGGAGGCGCTGACGCGGAGGCGTGCATATGAG 120
Db 61 CGGTCTGCGGAGCGGAGCTAGAGTAAAGGAGGCGCTGACGCGGAGGCGTGCATATGAG 120
QY 61 CGGTCTGCGGAGCGGAGCTAGAGTAAAGGAGGCGCTGACGCGGAGGCGTGCATATGAG 120
Db 61 CGGTCTGCGGAGCGGAGCTAGAGTAAAGGAGGCGCTGACGCGGAGGCGTGCATATGAG 120
QY 121 AGGCGAGGTGTCTGCTGCGAGCCCATATGACCCGCTGCGCTGCTGCTGCTGCTGCTG 180
Db 121 AGGCGAGGTGTCTGCTGCGAGCCCATATGACCCGCTGCGCTGCTGCTGCTGCTGCTG 180
QY 121 AGGCGAGGTGTCTGCTGCGAGCCCATATGACCCGCTGCGCTGCTGCTGCTGCTGCTG 180
Db 121 AGGCGAGGTGTCTGCTGCGAGCCCATATGACCCGCTGCGCTGCTGCTGCTGCTGCTG 180
QY 181 GGGGTGTCTCTGAGAGTCCCAAGAGACATGTTCCACAGGCTGTACACCCACGCGGA 240
Db 181 GGGGTGTCTCTGAGAGTCCCAAGAGACATGTTCCACAGGCTGTACACCCACGCGGA 240
QY 241 GAGTGTGCAAAAGCTGCAACTTGGGCGAAGGCGTGGCCGACCTGGGAGCCCAACGAG 300
Db 241 GAGTGTGCAAAAGCTGCAACTTGGGCGAAGGCGTGGCCGACCTGGGAGCCCAACGAG 300
QY 301 ACCGTGTGGAACCTGCTGCGAACAATTTACATTTCTCGAGTGTGAGGCGCCACTGAG 360
Db 301 ACCGTGTGGAACCTGCTGCGAACAATTTACATTTCTCGAGTGTGAGGCGCCACTGAG 360
QY 361 CGGTGCAAGCCGCGACCGAGTCCCTGCGGCTGCGAGAGCATGCTGCTGCTGCTGCTGAG 420
Db 361 CGGTGCAAGCCGCGACCGAGTCCCTGCGGCTGCGAGAGCATGCTGCTGCTGCTGCTGAG 420
QY 421 GCAGACGATGACGTGTGCGAGTGTGCTTATGCTTACACAGAGAGAGACACTGGCCAC 480
Db 421 GCAGACGATGACGTGTGCGAGTGTGCTTATGCTTACACAGAGAGAGACACTGGCCAC 480
QY 421 GCAGACGATGACGTGTGCGAGTGTGCTTATGCTTACACAGAGAGAGACACTGGCCAC 480
Db 421 GCAGACGATGACGTGTGCGAGTGTGCTTATGCTTACACAGAGAGAGACACTGGCCAC 480
QY 481 TGTGAGGCTTGCAGCGTGTGCGAGTGTGCTTATGCTTACACAGAGAGAGACTGGCCAC 540
Db 481 TGTGAGGCTTGCAGCGTGTGCGAGTGTGCTTATGCTTACACAGAGAGAGACTGGCCAC 540
QY 541 CAGAACACAGTGTGTGAAGAGTGTGCGAGAGGCGACATCTCAGACGAGAACCAACACG 600
Db 541 CAGAACACAGTGTGTGAAGAGTGTGCGAGAGGCGACATCTCAGACGAGAACCAACACG 600
QY 601 GACCGCTGCTTACCTGCGACGAGTGTGCGAGAGACACTGAGCGGCGAGTACGAGTGCAG 660
Db 601 GACCGCTGCTTACCTGCGACGAGTGTGCGAGAGACACTGAGCGGCGAGTACGAGTGCAG 660
QY 661 CCCTGCGCTGATGCTGAATGCGAAGAGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 661 CCCTGCGCTGATGCTGAATGCGAAGAGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 CCGGAGGCGCTGCGACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
Db 721 CCGGAGGCGCTGCGACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
QY 781 GACCTGTGACCCAGTACAGTGTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 781 GACCTGTGACCCAGTACAGTGTGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 841 GTAGTGAACCGCGGCGACCAACGAGAAC 867
Db 841 GTAGTGAACCGCGGCGACCAACGAGAAC 867

```

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RESULT 2
US-09-821-831-1
Sequence 1, Application US/09821631
Patent No. US20020137188A1
GENERAL INFORMATION:
APPLICANT: Bartlett, Perry Francis
APPLICANT: Coulson, Elizabeth Jane
APPLICANT: Fielden, Katrina
APPLICANT: Baca, Manuel
APPLICANT: Kilpatrick, Trevor

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APPLICANT: Surinder, Cheema
TITLE OF INVENTION: Method of Modularizing Cell Survival and
FILE REFERENCE: 3206,1001-000
CURRENT APPLICATION NUMBER: US/09/821,831
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/AU99/00860
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: AU PQ0701
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: AU PP6351
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3260
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic CDNA Sequence of Human
NAME/KEY: CDS
LOCATION: (115)...(1389)
US-09-821-831-1
Query Match 100.0%; Score 867; DB 9; Length 3260;
Best Local Similarity 100.0%; Pred. No. 4,8e-237;
Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGCTCCGGCGGGGAGAGGCGCTGGAGCCGATGCGAGTTCAAGCTCAGCCGAGACCAT 60
Db 1 ACAGCTCCGGCGGGGAGAGGCGCTGGAGCCGATGCGAGTTCAAGCTCAGCCGAGACCAT 60
QY 61 CGGTCTGCGGAGCGGAGCTAGAGTAAAGGAGGCGCTGACGCGGAGGCGTGCATATGAG 120
Db 61 CGGTCTGCGGAGCGGAGCTAGAGTAAAGGAGGCGCTGACGCGGAGGCGTGCATATGAG 120
QY 121 AGGCGAGGTGTCTGCTGCGAGCCCATATGACCCGCTGCGCTGCTGCTGCTGCTGCTG 180
Db 121 AGGCGAGGTGTCTGCTGCGAGCCCATATGACCCGCTGCGCTGCTGCTGCTGCTGCTG 180
QY 121 AGGCGAGGTGTCTGCTGCGAGCCCATATGACCCGCTGCGCTGCTGCTGCTGCTGCTG 180
Db 121 AGGCGAGGTGTCTGCTGCGAGCCCATATGACCCGCTGCGCTGCTGCTGCTGCTGCTG 180
QY 181 GGGGTGTCTCTGAGAGTCCCAAGAGACATGTTCCACAGGCTGTACACCCACGCGGA 240
Db 181 GGGGTGTCTCTGAGAGTCCCAAGAGACATGTTCCACAGGCTGTACACCCACGCGGA 240
QY 241 GAGTGTGCAAAAGCTGCAACTTGGGCGAAGGCGTGGCCGACCTGGGAGCCCAACGAG 300
Db 241 GAGTGTGCAAAAGCTGCAACTTGGGCGAAGGCGTGGCCGACCTGGGAGCCCAACGAG 300
QY 301 ACCGTGTGGAACCTGCTGCGAACAATTTACATTTCTCGAGTGTGAGGCGCCACTGAG 360
Db 301 ACCGTGTGGAACCTGCTGCGAACAATTTACATTTCTCGAGTGTGAGGCGCCACTGAG 360
QY 361 CGGTGCAAGCCGCGACCGAGTCCCTGCGGCTGCGAGAGCATGCTGCTGCTGCTGCTGAG 420
Db 361 CGGTGCAAGCCGCGACCGAGTCCCTGCGGCTGCGAGAGCATGCTGCTGCTGCTGCTGAG 420
QY 421 GCAGACGATGACGTGTGCGAGTGTGCTTATGCTTACACAGAGAGAGACACTGGCCAC 480
Db 421 GCAGACGATGACGTGTGCGAGTGTGCTTATGCTTACACAGAGAGAGACACTGGCCAC 480
QY 481 TGTGAGGCTTGCAGCGTGTGCGAGTGTGCTTATGCTTACACAGAGAGAGACTGGCCAC 540
Db 481 TGTGAGGCTTGCAGCGTGTGCGAGTGTGCTTATGCTTACACAGAGAGAGACTGGCCAC 540
QY 541 CAGAACACAGTGTGTGAAGAGTGTGCGAGAGGCGACATCTCAGACGAGAACCAACACG 600
Db 541 CAGAACACAGTGTGTGAAGAGTGTGCGAGAGGCGACATCTCAGACGAGAACCAACACG 600
QY 601 GACCGCTGCTTACCTGCGACGAGTGTGCGAGAGACACTGAGCGGCGAGTACGAGTGCAG 660
Db 601 GACCGCTGCTTACCTGCGACGAGTGTGCGAGAGACACTGAGCGGCGAGTACGAGTGCAG 660

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Db	661	CCCTGGGGCTGATGCTGAATGCGAAGAGATCCCTGGTTCATGGAATCCCAAGGTCTCAAGCCC	720
Qy	661	CCCTGGGGCTGATGCTGAATGCGAAGAGATCCCTGGTTCATGGAATCCCAAGGTCTCAAGCCC	720
Db	661	CCCTGGGGCTGATGCTGAATGCGAAGAGATCCCTGGTTCATGGAATCCCAAGGTCTCAAGCCC	720
Qy	721	CCGGAAGGGCTCCGACAGCAACAGCGCCAGACACCCAGAGGCTTAGGTCTCTCCAGAGCAA	780
Db	721	CCGGAAGGGCTCCGACAGCAACAGCGCCAGACACCCAGAGGCTTAGGTCTCTCCAGAGCAA	780
Qy	781	GACCTTGTATCCCACTCACTAGTGGCGGATATGTTGACCACTGTGATGGGAGAGTCCCAAGCTT	840
Db	781	GACCTTGTATCCCACTCACTAGTGGCGGATATGTTGACCACTGTGATGGGAGAGTCCCAAGCTT	840
Qy	841	GTAGTGACCCGCGGACCAACCGCAAC	867
Db	841	GTAGTGACCCGCGGACCAACCGCAAC	867

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RESULT 3
US-10-388-934-557
: Sequence 557, Application US/10388934
: Publication No. US20040005547A1
GENERAL INFORMATION:
APPLICANT: Boess, Franziska
APPLICANT: Suter-Dick, Laura
APPLICANT: Wolf, Detlef
TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
FILE REFERENCE: 21199
CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 02005336.9
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
SOFTWARE: PatentIn version 3.1
SEQ ID NO 557
LENGTH: 3259
TYPE: DNA
ORGANISM: Rattus norvegicus (NO. US20040005547A1way rat)
US-10-388-934-557

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Query Match	99.9%	Score 866	DB 15	Length 3259
Best Local Similarity	100.0%	Pred. No. 9.3e-237		
Matches 866	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1	CAGCTCCGGGCGGGCAGCAGAGCGCTGGAGGGGATCCGAGTTCAGCTCAGCGCAGACCATC	61
Db	1	CAGCTCCGGGCGGGCAGCAGAGCGCTGGAGGGGATTCGCAATTCAGCTCAGCGCAGACCATC	60
QY	62	GGTCTGGGAGCGGAGTGAAGTAAAGCGGAGCGCTGAAGCGCGAGGGGCTGCAATGAAGA	121
Db	61	GGTCTGGGAGCGGAGTGAAGTAAAGCGGAGCGCTGAAGCGCGAGGGGCTGCAATGAAGA	120
QY	122	GGGCAAGTGTGCTGCTGCTGACAGGCCATGGAACCGGCTGCGCTGTGTGTGTTGATTAG	181
Db	121	GGGCAAGTGTGCTGCTGCTGACAGGCCATGGAACCGGCTGCGCTGTGTGTGTTGATTAG	180
QY	182	GGGGTCTCTGTGAGAGGTGCGCAAGGAGACATGTTCCAGACGGCTGTGACCCCAAGCGGAG	241
Db	181	GGGGTCTCTGTGAGAGGTGCGCAAGGAGACATGTTCCAGACGGCTGTGACCCCAAGCGGAG	240
QY	242	AGTGTGCAAAAGCCTGCAACTTGTGGCGGAAGCGTGGCCAGGCCCTGCGGAGCCCAACGAG	301
Db	241	AGTGTGCAAAAGCCTGCAACTTGTGGCGGAAGCGTGGCCAGGCCCTGCGGAGCCCAACGAG	300
QY	302	CCGTGTGTGAACCTGTGCTTGAGCAATGTTACATTTCTCCGATGTGTGAGCGCCACTGAGC	361
Db	301	CCGTGTGTGAACCTGTGCTTGAGCAATGTTACATTTCTCCGATGTGTGAGCGCCACTGAGC	360
QY	362	CGTGCMAAGCCGTGCACACGAGTGTCTGGGCTGCACAGCATGTCCGCTCCCTGTGTGAAG	421
Db	361	CGTGCMAAGCCGTGCACACGAGTGTCTGGGCTGCACAGCATGTCCGCTCCCTGTGTGAAG	420

Qy	422	CAGACCATCACTGTCAGAGATGTGCTATGCTACTACACAGAACGAGAGACTGGCCACT	481
Db	421	CAGACATGCAGTGTGACAGATGTGCTATGCTACTACAGGACGAGAGACTGGCCACT	480
Qy	482	GTAAGGCTTCGACGGCTGTGCGAGGTGTGGGCTCGGGACTGTGTCTCTCCAGGACAAAC	541
Db	481	GTAAGGCTTCGACGGCTGTGCGAGGTGTGGGCTCGGGACTGTGTCTCTCCAGGACAAAC	540
Qy	542	AGAACACAGTGTGTGAAGTGTCCAGAGGGCACATACTCAGACGAAGCCAAACCACTGG	601
Db	541	AGAACACAGTGTGTGAAGTGTCCAGAGGGCACATACTCAGACGAAGCCAAACCACTGG	600
Qy	602	ACCCGTGCTTACCTTCGACAGGTGTGCGAGGACACTGAAGCCGACATTACGCGAGTGCACGC	661
Db	601	ACCCGTGCTTACCTTCGACAGGTGTGCGAGGACACTGAAGCCGACATTACGCGAGTGCACGC	660
Qy	662	CTCGGGCTATCTCTAAATGCCAAGAGATCCCTGTGTCCATGGATGCCAAGGTCTACGCCCC	721
Db	661	CTCGGGCTATCTCTAAATGCCAAGAGATCCCTGTGTCCATGGATGCCAAGGTCTACGCCCC	720
Qy	722	CGAGAGGCTCCACAGCAGCGCCACAGACCACAGAGCCTGAAGTTCCTCCAGAGCAAG	781
Db	721	CGAGAGGCTCCACAGCAGCGCCACAGACCACAGAGCCTGAAGTTCCTCCAGAGCAAG	780
Qy	782	ACCTTGTACCCAGTACAGTGTGCGGATATGTGTACCACTGTGATGTGGCAGCTCCAGGCTTG	841
Db	781	ACCTTGTACCCAGTACAGTGTGCGGATATGTGTACCACTGTGATGTGGCAGGCTCCAGGCTTG	840
Qy	842	TAGTGAACCGCGAGCAACCCGACAAAC	867
Db	841	TAGTGAACCGCGAGCAACCCGACAAAC	866

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RESULT 4
US-10-101-510-156
Sequence 156, Application US/10101510
Publication No. US20030148295A1
GENERAL INFORMATION:
APPLICANT: WANG, JACKSON
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101.510
CURRENT FILING DATE: 2002-03-20
PRIORITY APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 156
LENGTH: 3386
TYPE: DNA
ORGANISM: Homo sapiens
US-10-101-510-156

```

Query Match	72.6%;	Score 629.2;	DB 14;	Length 3386;
Best Local Similarity	85.0%;	Pred. No. 2.6e-169;		
Matches 716;	Conservative 0;	Mismatches 123;	Indels 3;	Gaps 1.

Oy 26 GAGGCCATCGCGATTACAGTCAAGCGACACATCGGTCTGCGAAGCGAGCTAGTAG 85
 Db 25 GGGGGGCGCTGAGACCGCACACGCGACGCCCCCATCATCCGCACAAACGAGCCGAGCTGG 84
 Oy 86 AAGCGAGAGCGCTGACGCCCGAGGCGCTGCATATGAGAGGGGACAGTGTCTGCTGCAGCGCCA 145
 Db 85 AAGTTCAGCGCTCCCGCGGAGCGAGCGCGC---GATGGGGGACAGGTGCCACCGCGCGGCCCA 141
 Oy 146 TGAGACGCGCTGCGCGCTGTGCTGTGATTTAGGGGTGTCCCTTGAGAGTGTCCAAAG 205
 Db 142 TGAACGGGCGCGGCGCTGTGCTGTGTGCTTTGAGGGTGTCCCTTGAGAGTGTCCAAAG 201
 Oy 206 AAGCATGTTTCACAGGCGCTGTACACCCACAGCGAGAGATGTGTGAAAGCTTGCAACTTG 255

Db 202 AGGCATGCCCAACAGGCGCTGTACACACAGCGGTGAGTGTCTGCAAGCCTTGCAACTGG 261
 QY 266 GCGAAGCGCTGGGCCCAAGCCTGCGAGCCAAACAGACCGTGTGTGACCTCTGACCA 325
 Db 262 GCGAGGCTGTGGGCCCAAGCCTTGTGAGCCAAACAGACCGTGTGTGAGCCCTGCTGACA 321
 QY 326 ATGTTACATTTCTCCGATGTGTGTGAGCGCACTGAGCCGTGTGCAAGCCGTGTGCAAGTGGC 385
 Db 322 GCGTGAAGTCTTCGACGTGTGTGAGCGACAGAGCCGTGTGCAAGCCGTGTGCAAGTGGC 381
 QY 386 TGGGCTGCGAGACAGTGTCCGCTCCCTGTGTGAGGCGACAGATGATGATGATGATGATG 445
 Db 382 TGGGCTGCGAGACAGTGTCCGCTCCCTGTGTGAGGCGACAGATGATGATGATGATGATG 441
 QY 446 CCTATGCTACTACCAAG 505
 Db 442 CCTACGCTACTACTACAG 501
 QY 506 TGGGCTGCGAG 565
 Db 502 GCGGCTGCGAG 561
 QY 566 CAGAGGCGACATCTAGACAG 625
 Db 562 CCGAGGCGACATCTAGACAG 621
 QY 626 GCGAG 685
 Db 622 GCGAG 681
 QY 686 AGATCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 745
 Db 682 AGATCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 741
 QY 746 CCGAG 805
 Db 742 CCGAG 801
 QY 806 ATATGATGACCACTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 865
 Db 802 GTGTGTGACCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 861
 QY 866 AC 867
 Db 862 AC 863

RESULT 5

US-10-116-275-209
 ; Sequence 209, Application US/10116275
 ; Publication No. US20030211476A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Elan Pharmaceutical Technology
 ; APPLICANT: O'Mahony, Daniel J.
 ; APPLICANT: Brayden, David
 ; APPLICANT: Byrne, Daragh
 ; APPLICANT: Lambkin, Imelda
 ; APPLICANT: Higgins, Lisa
 ; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
 ; FILE REFERENCE: E1067/20087
 ; CURRENT APPLICATION NUMBER: US/10/116,275
 ; NUMBER OF SEQ ID NOS: 349
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 209
 ; LENGTH: 3386
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-116-275-209

Query Match 72.6%; Score 629.2; DB 15; Length 3386;
 Best Local Similarity 85.0%; Pred. No. 2,66-169;

Matches 716; Conservative 0; Mismatches 123; Indels 3; Gaps 1;
 QY 26 GAGAGCATGCGAGTTGAGCTCAGCGAGAGACCATGATGCTGTGCGAGCGGACTGAGCTAG 85
 Db 25 GAGAGGCGCTGAGCGAGCGAGCGAGCGGAGCCCATGATGCTGCGAAGCGGAGCGGACTGAG 84
 QY 86 AAGCGAGCGCTGAGCGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 145
 Db 85 AAGCGAGCGCTGAGCGCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 141
 QY 146 TGGACCGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 205
 Db 142 TGGACCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 201
 QY 206 AGCATGTTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 265
 Db 202 AGGCATGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 261
 QY 266 GCGAAGGCGTGGGCCCAAGCCTGCGAGCCAAACAGACCGTGTGTGACCTCTGACCA 325
 Db 262 GCGAGGCTGTGGGCCCAAGCCTTGTGAGCCAAACAGACCGTGTGTGAGCCCTGCTGACA 321
 QY 326 ATGTTACATTTCTCCGATGTGTGTGAGCGCACTGAGCCGTGTGCAAGCCGTGTGCAAGTGGC 385
 Db 322 GCGTGAAGTCTTCGACGTGTGTGAGCGACAGAGCCGTGTGCAAGCCGTGTGCAAGTGGC 381
 QY 386 TGGGCTGCGAG 445
 Db 382 TGGGCTGCGAG 441
 QY 446 CCTATGCTACTACCAAG 505
 Db 442 CCTACGCTACTACTACAG 501
 QY 506 TGGGCTGCGAG 565
 Db 502 GCGGCTGCGAG 561
 QY 566 CAGAGGCGACATCTAGACAG 625
 Db 562 CCGAGGCGACATCTAGACAG 621
 QY 626 GCGAG 685
 Db 622 GCGAG 681
 QY 686 AGATCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 745
 Db 682 AGATCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 741
 QY 746 CCGAG 805
 Db 742 CCGAG 801
 QY 806 ATATGATGACCACTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 865
 Db 802 GTGTGTGACCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 861
 QY 866 AC 867
 Db 862 AC 863

RESULT 6

US-09-918-995-7905
 ; Sequence 7905, Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseed, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FILE REFERENCE: FROM VARIOUS CDNA LIBRARIES
 ; CURRENT APPLICATION NUMBER: US/09/918,995

PUBMED
 11042159
 3
 Shibata, K., Itch, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Komori, H., Akiyama, J., Nishi, K., Kitajima, T., Tashiro, H., Itch, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishimura, T., Harada, A.,
 Yamamoto, R., Matsumoto, K., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubara, K.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multichannel sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 JOURNAL
 MEDLINE
 20530913
 11076861
 4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 3399)
 JOURNAL
 REFERENCE
 AUTHORS
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
 Hori, P., Imocani, K., Ishii, Y., Itch, M., Kagawa, I., Kanakawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komori, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N.,
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 Sorabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akaira, S.,
 Tanaka, Y., Tanaka, T., Tomaru, A., Toy, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-Jul-2001) Yoshitake Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tezumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 COMMENT
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in Riken
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/
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 putative"
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[illegible]

Fri Mar 12 17:00:18 2004

us-09-821-831-3.rst

Page 5

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ACCESSION
CB586038
VERSION
CB586038.1 GI:29530079
KEYWORDS
EST.
SOURCE
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ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 584)
Amgen EST Program.
TITLE
Amgen Rat EST Program
JOURNAL
Unpublished (2003)
COMMENT
Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
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/db_xref="taxon:10116"
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from internal pSPORT vector"
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Matches 562; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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62 GCTCTGCGGAGCGGAGCTGAGCGGAGCGCGCTGAGCGCGGAGCGCGGAGCGCGATGAGA 121
80 GCTCTGCGGAGCGGAGCTGAGCGGAGCGCGCTGAGCGCGGAGCGCGGAGCGCGATGAGA 139
122 GGGCAGAGTCTCTCGCAGCGCGCATGAGCGCGCTGCGCTCTGCTGCTGATTCAG 181
140 GGGCAGAGTCTCTCGCAGCGCGCATGAGCGCGCTGCGCTCTGCTGCTGATTCAG 199
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242 AGTGTGCAAAAGCCGCAACTTGGCGGAGGCGTGGCCAGCCCTGCGGAGCCCAACAGA 301
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320 CCGTGTGTGAACCTGCTGCAATGTTTACATTCTCCGATGTGTGAGGCCCACTGAGC 379
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542 AGAACAAGTGTGTGAAGAGTGC 566
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RESULT 6
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LOCUS
DEFINITION
BB630380 RIKEN full-length enriched, 6 days neonate skin mus
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ACCESSION
BB630380
VERSION
BB630380.1 GI:16467363
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 645)
Arikawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, F.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takeda, H.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arikawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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URL: http://genome.resgsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayashizaki, Y., Sugihara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagti, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Matsui, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsushita, S., Kawai, T., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multichannel sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugihara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamanka, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.resgsc.riken.go.jp) for
further details.
e mouse tissues.

FEATURES
source

1..645
Location/Qualifiers
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'] GAGAGAGAGAGATCCAGAGACTCTTTTCTTTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5'] GAGAGAGAGATCTCGATTAATTAATTCCTCCCTCCCTCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda phage I."

ORIGIN

Query Match 59.0%; Score 511.8; DB 10; Length 645;
Best local Similarity 91.9%; Pred. No. 6, 1e-104;
Matches 567; Conservative 0; Mismatches 37; Indels 13; Gaps 2;

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DB 82 CAGCATCGTCTCCGAGAGCGGAGCTAGAGAGCGGAGCGCTGAGCGCGAGCGGAGCA 141
QY 115 ATGAGAGAGGAGAGTCTCTGCTGAGCGCATGAGCGGCTGCGC-----CTGCTGTG 168
DB 142 ATGAGAGAGGAGAGTCTCTGCTGAGCGCGCATGAGCGGCTGCGCTGCTGCTGTG 201
QY 169 CTGCTGATCTCTGAGGCTGCTCTGAGAGTCCAGAGAGAGCATGTTCCAGAGCGCTGAC 228
DB 202 CTGCTGCTCTGAGGCTGCTCTGAGAGTCCAGAGAGCATGTTCCAGAGCGCTGAC 261
QY 229 ACCCAGAGGAGAGTCTGCTCAAGGCTTCACTTGGGCGAAGGCGTGGCCAGCCCTGC 288
DB 262 ACCCAGAGGAGAGTCTGCTCAAGGCTTCACTTGGGCGAAGGCGTGGCCAGCCCTGC 321
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DB 382 AGGCGCAGAGAGTCTGCTCAAGGCTTCACTTGGGCGAAGGCGTGGCCAGCCCTGC 441
QY 409 CCTGTGTGTGAGAGAGTCTGCTCAAGGCTTCACTTGGGCGAAGGCGTGGCCAGCCCTGC 468
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LOCUS BB655751 RIKEN full-length enriched, 12 days embryo spinal ganglion
DEFINITION Mus musculus cDNA clone D130022N18 5', mRNA sequence.
ACCESSION BB655751
VERSION BB655751.1 GI:16489579
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 622)
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hasegawa, T., Hara, A., Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kondo, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ono, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takehashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

TITLE

JOURNAL

Unpublished (2001)
Contact: Yoshihide Hayashizaki

COMMENT

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Fax: 81-45-503-9216

Email: genome-resseq@riken.go.jp,
URL: http://genome.gsc.riken.go.jp/

Carninci, P., Shibata, Y., Hayashizaki, Y., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuzawa, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamashita, T., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
e mouse tissues.

FEATURES

Source

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/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'] GAGAGAGAGAGATCCAGAGACTCTTTTCTTTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'] GAGAGAGAGATCTCGATTAATTAATTCCTCCCTCCCTCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda phage I."

ORIGIN

Query Match 58.2%; Score 504.4; DB 10; Length 622;
 Best Local Similarity 92.5%; Pred. No. 2.7e-102;
 Matches 556; Conservative 0; Mismatches 32; Indels 13; Gaps 2;

2 CAGCTCCGCGCGGAGCAGAGCCGCTGAGCCGATCGCAATTCAGTCA-----GCGCAG 54
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 82 CACCACTGGCTCTGCGGAGCGGAGCTGAGCTAGAAAGCGGAGCCCTGACCGCGGAGCGGCA 141
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 142 ATGAGGAGGAGGAGTGTCTGCTGCAAGCGGATGAGCCGCTGCGC-----CTGCTGCTG 201
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 409 CCCTGTGTGAGAGCAGACGATGAGTGTGCAATGTGCTTACTTACAGAGCGAG 468
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 469 GAGATGTGAGAGCAGACGATGAGTGTGCAATGTGCTTACTTACAGAGCGAG 528
 502 GAGATGTGAGAGCAGACGATGAGTGTGCAATGTGCTTACTTACAGAGCGAG 561
 529 TSCCAGAGCAAAACAGAAACAGTGTGTGAAGTGTCCAGAGGAGCAATTCAGAGCGAA 588
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 622 G 622

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 VERSION BQ718679.1 GI:21857576
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 942)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabds-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.jnl.gov
 plate: ILNL1581 row: P column: 17
 High quality sequence stop: 543.
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 5'-GACTAGTCTAGATCGGAGCGGCGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.9 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine); available through Life
 Technologies."

ORIGIN
 Query Match 58.2%; Score 504.2; DB 13; Length 942;
 Best Local Similarity 84.0%; Pred. No. 3.8e-102;
 Matches 582; Conservative 0; Mismatches 108; Indels 3; Gaps 1;

36 GCAATTCAGTCCGCGGAGCAGACATGAGTGTGCGGAGCGGAGCTGAGCTGAGAGCGAGG 95
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 421 CTACCGAGGAG 480
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nrhy7-00043-a7 5', mRNA sequence.
ACCESSION CB725789
VERSION CB725789.1 GI:29792714
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ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 490)
REFERENCE 1 (bases 1 to 490)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
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FEATURES
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/clone_1lb="nrhy7 (10850)"
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat
hypothalamus adult female Wistar rat avg. Insert size 2.3
kb fraction 6 and 7"

ORIGIN
Query Match 55.0%; Score 477.2; DB 14; Length 490;
Best Local Similarity 99.4%; Pred. No. 2,9e-96;
Matches 479; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 CAGCTCCGGGGCAGAGGCGCTGAGCGCATGCAATTCACTCAGCGCAGCAACCATC 61
Db 9 CAGCTCCGGGGCAGAGGCGCTGAGCGCATGCAATTCACTCAGCGCAGCAACCATC 68
QY 62 GGTCTGGAGAGGAGCTGAGCTAGAAAGCGAGCGCTGAGCGCGGAGCGCTGCAATGAGA 121
Db 69 GGTCTGGAGAGGAGCTGAGCTAGAAAGCGAGCGCTGAGCGCGGAGCGCTGCAATGAGA 128
QY 122 GGGCAGGTGCTGCTGCTGAGCGCATGAGACCGAGTGGCTGCTGCTGCTGCTGATTTG 181
Db 129 GGGCAGGTGCTGCTGAGCGCATGAGACCGAGTGGCTGCTGCTGCTGCTGATTTG 188
QY 182 GGGAGTCTCTGAGAGGAGGAGAGACATGTTCCAGAGCGCTGTAACCCACAGGGAG 241
Db 189 GGAATGCTCTTGAAGGTGAGAGAGACATGTTCCAGAGCGCTGTAACCCACAGGGAG 248
QY 242 AGTCTGCAAAAGCTGCAACTTGGCGAAGCGTGGCCCAAGCCCTGCGAGCCCAACAGA 301
Db 249 AGTCTGCAAAAGCTGCAACTTGGCGAAGCGTGGCCCAAGCCCTGCGAGCCCAACAGA 308
QY 302 CCGGTGTGAACCTGCTGAGACATGTTCAATTCCGATGAGAGGAGGAGCACTGAGC 361
Db 309 CCGGTGTGAACCTGCTGAGACATGTTCAATTCCGATGAGAGGAGGAGCACTGAGC 368
QY 362 CGTGAAGCGGTGACCGAGTGCCTGGCGCTGAGAGACATGTCGCTCCCTGTGTGAGG 421
Db 369 CGTGAAGCGGTGACCGAGTGCCTGGCGCTGAGAGACATGTCGCTCCCTGTGTGAGG 428

QY 422 CAGACATGAGATGTGAGATGAGCTATGGCTATGAGTACCAAGAGAGAGAGACTGGCCACT 481
Db 429 CAGACATGAGATGTGAGATGAGCTATGAGTACCAAGAGAGAGAGACTGGCCACT 488
QY 482 GT 483
Db 489 GT 490

RESULT 10
CB716157 517 bp mRNA linear EST 10-APR-2003
LOCUS CB716157
DEFINITION AMGNNUC:NRHY5-00132-C2-A W Rat hypothalamus (10471) Rattus
norvegicus cDNA clone nrhy5-00132-c2 5', mRNA sequence.
ACCESSION CB716157
VERSION CB716157.1 GI:29773305
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 517)
REFERENCE 1 (bases 1 to 517)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00132 row: c column: 2.

FEATURES
source
1..517
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrhy5-00132-c2"
/clone_1lb="W Rat hypothalamus (10471)"
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat
hypothalamus adult female Wistar rat avg. Insert size 2.3
kb fraction 6 and 7"

ORIGIN
Query Match 55.0%; Score 477.2; DB 14; Length 517;
Best Local Similarity 97.4%; Pred. No. 3e-96;
Matches 485; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 2 CAGCTCCGGGGCAGAGGCGCTGAGCGCATGCAATTCACTCAGCGCAGCAACCATC 61
Db 20 CAGCTCCGGGGCAGAGGCGCTGAGCGCATGCAATTCACTCAGCGCAGCAACCATC 79
QY 62 GGTCTGGAGAGGAGCTGAGCTAGAAAGCGAGCGCTGAGCGCGGAGCGCTGCAATGAGA 121
Db 80 GGTCTGGAGAGGAGCTGAGCTAGAAAGCGAGCGCTGAGCGCGGAGCGCTGCAATGAGA 129
QY 122 GGGCAGGTGCTGCTGAGCGCATGAGACCGAGTGGCTGCTGCTGCTGCTGATTTG 181
Db 140 GGGCAGGTGCTGCTGAGCGCATGAGACCGAGTGGCTGCTGCTGCTGATTTG 189
QY 182 GGGAGTCTCTGAGAGGAGGAGAGACATGTTCCAGAGCGCTGTAACCCACAGGGAG 241
Db 200 GGAATGCTCTTGAAGGTGAGAGAGACATGTTCCAGAGCGCTGTAACCCACAGGGAG 259
QY 242 AGTCTGCAAAAGCTGCAACTTGGCGAAGCGTGGCCCAAGCCCTGCGAGCCCAACAGA 301
Db 260 AGTCTGCAAAAGCTGCAACTTGGCGAAGCGTGGCCCAAGCCCTGCGAGCCCAACAGA 319
QY 302 CCGGTGTGAACCTGCTGAGACATGTTCAATTCCGATGAGAGGAGGAGCACTGAGC 361
Db 320 CCGGTGTGAACCTGCTGAGACATGTTCAATTCCGATGAGAGGAGGAGCACTGAGC 379
QY 362 CGTGAAGCGGTGACCGAGTGCCTGGCGCTGAGAGACATGTCGCTCCCTGTGTGAGG 421

Query	Db	Score	Length	Matches	Conservative	Mismatches	Indels	Gaps
1	MRBAGACGAMDRRLRLILLILIGVSSGGAKENCGTGLYTHSGECCRAKNLGGVAPPCGA	100.0%	251	251	0	0	0	0
1	MRBAGACGAMDRRLRLILLILIGVSSGGAKETCSGLYTHSGECCRAKNLGGVAPPCGA	100.0%	251	251	0	0	0	0
61	NCIVCEPCLDNWTFSVDVSNATEPCPKCTECLGLQSMAPCYEADAVCAVGYQDEET	100.0%	251	251	0	0	0	0
61	NCIVCEPCLDNWTFSVDVSNATEPCPKCTECLGLQSMAPCYEADAVCAVGYQDEET	100.0%	251	251	0	0	0	0
121	GHCBAQSVCEVSGGLVFCQDKQNVCECECGTQSDANVNDPCLCTVCEPTEQLRE	100.0%	251	251	0	0	0	0
121	GHCBAQSVCEVSGGLVFCQDKQNVCECECGTQSDANVNDPCLCTVCEPTEQLRE	100.0%	251	251	0	0	0	0
181	CTFMADABCEIIFGRWIPRSTPPESDSSTAPSTCEPEVPPQDLVPSVADMTTMMGSS	100.0%	251	251	0	0	0	0
181	CTFMADABCEIIFGRWIPRSTPPESDSSTAPSTCEPEVPPQDLVPSVADMTTMMGSS	100.0%	251	251	0	0	0	0
241	QPVVTRGTTDN 251	100.0%	251	251	0	0	0	0
241	QPVVTRGTTDN 251	100.0%	251	251	0	0	0	0

	XX	PS	Disclosure; Page 69-70; 80pp; English.
	XX	PT	Novel nucleic acids encoding a peptide capable of facilitating the death
	XX	PT	of a cell, useful for antagonizing cell death signal function and
	XX	PT	promoting cell death, e.g. for treating cancer.
	XX	PI	Surinder C;
	XX	PI	Bartlett PF, Coulson EJ, Fieldaw K, Baca M, Kilpatrick T;
	XX	PA	(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
	XX	DR	WPI; 2000-328933/28.
	XX	DR	N-PDB; AAM09356.
	CC	CC	This is the human p75 neurotrophin receptor (p75-NTR). p75-NTR is
	CC	CC	multifunctional and is capable of acting as a death receptor. Elevated
	CC	CC	p75-NTR expression results in increased death in vitro and in vivo. It
	CC	CC	has been determined that the death signal is not the cytoplasmic motif
	CC	CC	known as the death domain, but is a region adjacent the membrane domain
	CC	CC	on p75-NTR. Identification of this region provides an opportunity to
	CC	CC	modulate cell survival by antagonising the death signalling region or
	CC	CC	promoting apoptosis by providing cells with the genetic material to
	CC	CC	express the death signalling region adjacent, proximal, or otherwise
	CC	CC	juxtaposed or associated membrane of a cell or to express the death
	CC	CC	signalling region in multicentric form. The polypeptides and methods of the
	CC	CC	invention are useful for inhibiting, reducing or antagonizing p75-NTR-
	CC	CC	mediated death signals in neural cells. In particular, the methods are
	CC	CC	used for the treatment or prophylaxis of disease conditions associated
	CC	CC	with neutral death or where cell death is to be promoted such as in
	CC	CC	treating or preventing cancer growth and/or development. Other diseases
	CC	CC	capable of treatment include neurodegenerative diseases, such as cerebral
	CC	CC	palsy, trauma induced paralysis, vascular ischemia associated with
	CC	CC	stroke, neural tumors, motorneurone diseases, Parkinson's disease and
	CC	CC	Huntington's disease, Alzheimer's disease, multiple sclerosis and
	CC	CC	peripheral neuropathies associated with diabetes, heavy metal or alcohol
	CC	CC	toxicity, renal failure, and/or infectious diseases such as Herpes,
	CC	CC	rubella, measles, chicken pox, HIV and HTLV-1 (all claimed). The methods
	CC	CC	are also useful for treating neurons or glia damaged by trauma or disease
	CC	CC	(claimed). Animals which can be treated include humans, livestock
	CC	CC	animals, laboratory test animals, companion animals, and captive wild
	CC	CC	animals
	XX	XX	Sequence 425 AA:
	XX	XX	Query Match 100.0%; Score 1387; DB 3; Length 425;
	XX	XX	Best Local Similarity 100.0%; Pred. No. 2,1e-99;
	XX	XX	Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY			1 MRAGAAGCANDRLLLLLLLILGYSSGGAATCTGTHTSGGCCAKNIGBVAPPCA 60
Db			1 MRAGAAGCANDRLLLLLLLILGYSSGGAATCTGTHTSGGCCACNIGBSVAPPCA 60
OY			61 NOTVCBPCLDNTFTSDVVSATEPKPCTCECLGLQSMAPCVEADDAVCRCAVYODEBT 120
Db			61 NOTVCBPCLDNTFTSDVVSATEPKPCTCECLGLQSMAPCVEADDAVCRCAVYODEBT 120
OY			121 GHCEACSVCEVSSGLVESCQOKONTVCBECPBGITYSBANHVDPCLPCTVCEBTEQLRE 180
Db			121 GHCEACSVCEVSSGLVFSCQOKONTVCBECPBGITYSBANHWVPCLPCTVCEBTEQLRE 180
OY			181 CTPEWADAACEEIPGRMIPRSTPPESGSTAPSTOEPEVPPEODLVESTADMTVTMGSS 240
Db			181 CTPEWADAEEELPGRMIPRSTPPESGSTAPSTOEPEVPPEODLVSTADVMTVTMGSS 240
OY			241 QPVVTRGITDN 251
Db			241 QPVVTRGITDN 251

ID AAE21671 standard; protein; 425 AA.

XX AAE21671,

XX AAE21671,

XX 16-JUL-2002 (first entry)

XX DE Rat neurotrophic receptor (p75NTR) protein.

XX KM Rat; diabetic neuropathy; therapy; neurotrophic receptor; p75NTR;

XX KW drug screening; receptor.

XX OS Rattus sp.

XX PN MO200218955-A1.

XX PD 07-MAR-2002.

XX PF 29-AUG-2001; 2001MO-GS003859.

XX FR 01-SEP-2000; 2000GB-00021609.

XX PA (UTMA-) UNIV VICTORIA MANCHESTER.

XX PI Tomlinson DR;

XX DR WPI; 2002-332976/36.

XX PS

PT Detecting neuropathy, evaluating effect/efficacy of a drug for treating

PT PT neuropathy or screening compounds to assess their side effects causing

PT PT neuropathy, by detecting 75 kDa Neurotrophic Receptor in patient sample.

PS Disclosure; Fig 2; 33pp; English.

XX The invention relates to an in vitro test for neuropathy, for evaluating

CC whether a subject will benefit from a putative drug for treating

CC CC neuropathy. The method comprising detecting for the presence of a 75 kDa

CC CC neurotrophic receptor (p75NTR) in a body fluid sample. The invention is

CC used for diagnosing neuropathy, particularly diabetic neuropathy,

CC screening the efficacy of a putative drug for treating neuropathy, for

CC evaluating whether or not a subject will benefit from a putative drug for

CC treating neuropathy, for screening a compound to assess whether or not a

CC compound causes neuropathy, monitoring the health status of a subject

CC with or at risk of developing neuropathy and testing whether or not a

CC subject is complying with therapeutic regime for treating diabetes. The

CC method is also useful for making a detailed analysis such as a clinical

CC trial of a drug targetted at diabetic neuropathy. The present sequence is

CC rat p75NTR protein

XX XX

SQ Sequence 425 AA:

Query March 100.0%; Score 1387; DB 5; Length 425;

Best Local Similarity 100.0%; Pred. No. 2,1e-99;

Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Y 1 MRPAGAAACSMADRLRLILLILIIIGVSSGGAKETCGTGLYTHSGECCKA CNIAGEVAOPCGA 60

Y 1 MRPAGAACSMADRLRLILLILIIIGVSSGGAKETCGTGLYTHSGECCKA CNIAGEVAOPCGA 60

Y 61 NQTVCEPCLDNVTFSSVVSATBPCRPCTCCLGLOMSAPCYEADADAYCRCAHYGOOEI 120

Y 61 NQTVCEPCLDNVTFSSVVSATBPCRPCTCCLGLOMSAPCYEADADAYCRCAHYGOOEI 120

Y Db 61 NQTVCEPCLDNVTFSSVVSATBPCRPCTCCLGLOMSAPCYEADADAYCRCAHYGOOEI 120

Y Y 121 GHCEAGCVGVGSGLVFSQCDDKONTVCBCECPGTYSDEANHVDPCLCTVCEDTEROLR 180

Y Y 121 GHCEAGCVGVGSGLVFSQCDDKONTVCBCECPGTYSDEANHVDPCLCTVCEDTEROLR 180

Y Db 121 GHCEAGCVGVGSGLVFSQCDDKONTVCBCECPGTYSDEANHVDPCLCTVCEDTEROLR 180

Y Y 181 CTPEADACEEIEGRWIPSTPEEGDSITAPETOEPVPPODLPVSTVADMVTYWGS 240

Y Y 181 CTPEADACEEIEGRWIPSTPEEGDSITAPETOEPVPPODLPVSTVADMVTYWGS 240

Y Db 181 CTPEADACEEIEGRWIPSTPEEGDSITAPETOEPVPPODLPVSTVADMVTYWGS 240

Y Y 241 QPVVTTGTTDN 251

DB 241 QPVTREGTDM 251

RESULT 4
ADBB81367
ID ADBB81367 standard; protein; 425 AA.
XX ADBB81367;
XX 04-DEC-2003 (first entry)
XX Rat nerve growth factor receptor p75 protein.
XX
XX rat; CARD-3; CARD-4; caspase recruitment domain; apoptosis; p75;
XX tumour necrosis factor; TNF; neutrophin receptor; cancer;
XX autoimmune disorder; systemic lupus; immune mediated glomerulonephritis;
XX viral infection; neurological; retinitis pigmentosa; haematologic;
XX chronic neutropenia; myocardial infarction; stroke; RIP; RICK; CARDIAX.
XX
XX Rattus sp.
XX US2002061833-A1.
XX 23-MAY-2002.
XX 26-DEC-2000; 2000US-00748537.
XX 06-FEB-1998; 98US-00019942.
XX 17-JUN-1998; 98US-00099041.
XX (BERT/) BERTIN J.
XX (CHAO/) CHAO M V.
XX Bertin J, Chao MV;
XX WPI; 2003-657125/62.
XX
XX Detecting compounds which alter binding of the caspase recruitment domain
XX (CARD) of CARD-3 polypeptide to the neutrophin receptor p75 is useful
XX to provide compounds for treating CARD-3 mediated disorders.
XX
XX Disclosure; Fig 14; 40pp; English.
XX
XX This invention relates to two novel genes CARD-3 and CARD-4 (caspase
XX recruitment domains) which are mediators of apoptosis and are useful in
XX the identification of compounds that modulate apoptosis. Specifically,
XX CARD-3 (also known as RIP2, RICK and CARDIAX) is known to be a mediator
XX of p75 (a member of the tumour necrosis factor (TNF) family), and is
XX believed to provide the switch for cell survival and cell death decisions
XX mediated by this p75 neutrophin receptor. Accordingly these genes, and
XX the proteins encoded thereof, are linked to certain disorders associated
XX with an increased number of cells surviving and proliferating when
XX apoptosis is inhibited. These include cancer, autoimmune disorders e.g.
XX systemic lupus and immune mediated glomerulonephritis, viral infections
XX such as those caused by the herpesvirus, neurological disorders such as
XX retinitis pigmentosa, haematologic diseases including chronic
XX neutropenia, as well as myocardial infarction and strokes. The present
XX invention further describes a novel method for determining whether a test
XX compound alters the binding of CARD-3 to p75, which comprises measuring
XX the binding of a polypeptide containing the CARD domain of CARD-3 to a
XX polypeptide comprising the death domain of p75 in the presence and
XX absence of the test compound, and determining if binding is altered. This
XX polypeptide is the rat nerve growth factor receptor protein sequence of
XX the invention.
XX
XX Sequence 425 AA;
XX
XX Query Match 100.0%; Score 1387; DB 7; Length 425;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-99;
XX Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRGAGACASANDRRLILILILGVSAGGAKATCGTGLYTHSGECCAKNLGAGVAQPCGA 60

DB 1 MRRAGAACSMRRLRLILLIIGVSSGAKETCTGLYTHSGECCACNLGEGVAPCGA 60
 QY 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQSMAPCVADAVCRCAVGYODEET 120
 DB 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQSMAPCVADAVCRCAVGYODEET 120
 QY 121 GHCEACSVCEVSGLVFSCQDKONTVCCECPGEGTSDENAHVDPCLPCTVCEDETERQRE 180
 DB 121 GHCEACSVCEVSGLVFSCQDKONTVCCECPGEGTSDENAHVDPCLPCTVCEDETERQRE 180
 QY 181 CTPWADACEEIPGRNIPRSTPEGSDSTAPSTOEVEVPEDDLVPSIVADMTVMGSS 240
 DB 181 CTPWADACEEIPGRNIPRSTPEGSDSTAPSTOEVEVPEDDLVPSIVADMTVMGSS 240
 QY 241 QPVYTRGTTDN 251
 DB 241 QPVYTRGTTDN 251

RESULT 5

ID ADE63294 standard; protein; 425 AA.

AC ADE63294;

DT 29-JAN-2004 (first entry)

DE Rat Protein P07174, SEQ ID NO 9231.

KM Rat, pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

PN MO2003016475-A2.

FD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; P07174.

PT New composition comprising two or more isolated polypeptides, useful for

XX preparing a medicament for treating pain in an animal.

PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

SC Sequence 425 AA;

Query Match 100.0%; Score 1387; DB 7; Length 425;
 Best Local Similarity 100.0%; Pred No. 2, 1e-99;
 Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRAGAACSMRRLRLILLIIGVSSGAKETCTGLYTHSGECCACNLGEGVAPCGA 60

DB 1 MRRAGAACSMRRLRLILLIIGVSSGAKETCTGLYTHSGECCACNLGEGVAPCGA 60

QY 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQSMAPCVADAVCRCAVGYODEET 120

DB 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQSMAPCVADAVCRCAVGYODEET 120

QY 121 GHCEACSVCEVSGLVFSCQDKONTVCCECPGEGTSDENAHVDPCLPCTVCEDETERQRE 180

DB 121 GHCEACSVCEVSGLVFSCQDKONTVCCECPGEGTSDENAHVDPCLPCTVCEDETERQRE 180

QY 181 CTPWADACEEIPGRNIPRSTPEGSDSTAPSTOEVEVPEDDLVPSIVADMTVMGSS 240

DB 181 CTPWADACEEIPGRNIPRSTPEGSDSTAPSTOEVEVPEDDLVPSIVADMTVMGSS 240

QY 241 QPVYTRGTTDN 251

DB 241 QPVYTRGTTDN 251

RESULT 6

ID AAY33483 standard; protein; 427 AA.

AC AAY33483;

DT 19-JAN-2000 (first entry)

DE Human neutrophin receptor p75NTR protein.

XX Proapoptotic; dependence domain; p75NTR; androgen receptor; DCC;

XX huntingtin polypeptide; Machado-Joseph disease; SCA1; SCA2; SCA6;

XX atrophin-1; cell death; apoptosis; Huntington's disease; head trauma;

XX Alzheimer's disease; Kennedy's disease; spinocerebellar ataxia; stroke;

XX dentatorubropallidoluysian atrophy; cell proliferation; cell survival;

XX neoplastic; malignant; autoimmune; fibrotic.

OS Homo sapiens.

PM WO9945944-A1.

PD 16-SEP-1999.

PF 11-MAR-1999; 99WO-US005250.

PR 12-MAR-1998; 98US-0004186.

PA (BURN-) BURNHAM INST.

XX Bredesen DE, Rabizadeh S;

XX WPI; 1999-561617/47.

DR N-PSDB; AA223423.

XX

Query	DB	Score	Length	DB 2	Length 427	Best Local Similarity	90.7%	Pred. No. 2,6e-88	Matches 225	Conservative 6	Mismatches 17	Indels 0	Gaps 0
4	AGAACGAMRLRLILLILLIVSSGGAKETCSGLYTHSGECCXCNLGEVAPCGANOT	63											
3	AGATGRAMGPRILLILLIVSLVGGAKKCPGLYTHSGECCXCNLGEVAPCGANOT	62											
64	VCEPCIDNVTFSDDVSNATEPCPKPCTECGLGOSMAPCVBADDAVCRCAVGYODEBTGHC	123											
63	VCEPCIDSVTFSPDVSVAATEPCPKPCTECVGLGOSMAPCVBADDAVCRCAVGYODEBTGRC	122											
124	EACSGVENSGVLFSCODKONTVCBCEGEGTSPDANHVDPCLCTVCEPTEBOLAECP	183											
123	EACRVCBAGSLVFSQDKONTVCBCEPGLTSDANHVDPCLCTVCEPTEBOLAECTR	182											
184	MADACEEIPGRNIPRSTPPESGDSSTAPSTGEPEVPEQDILVPSVTADMTTWGSSQPV	243											
183	MAADACEEIPGRNITRSTPPESGDSSTAPSTGEPEAPPEQDILASTAGVTTWAGSSQPV	242											
244	VTEGTTDN 251												
243	VTRGTTDN 250												

RESULT 7
AAB50894 ID AAB50894 standard; protein; 427 AA.
AAB50894; 19-MAR-2001 (first entry)
Human NGFR p75.
Human; TR10 receptor; cytosolic; immunosuppressive; neuroprotective; anti-inflammatory; anti-HIV; antiparkinsonian; nociceptive; cardiac; vasoregulatory; antiallergic; antidiabetic; vulnery; ophthalmological; antiviral; antibacterial; antifungal; antiparasitic; gene therapy; tumour necrosis factor receptor; cancer; leukaemia; autoimmune disorder; apoptosis; cardiovascular disorder; inflammatory disease; wound; infection; neurological disease; NGFR; nerve growth factor receptor; protein coordinate data.
Homo sapiens.
W0300673321-AL.
07-DEC-2000.

XX	26-MAY-2000; 2000MO-US014554.	FE
PR	28-MAY-1999; 99US-0136786P.	PR
PR	07-JUL-1999; 99US-0142563P.	PR
PR	15-JUL-1999; 99US-0144023P.	PR
XX	(HUMA-) HUMAN GENOME SCI INC.	XX
PA		PA
PI	Rosen CA, N1 J;	PI
XX		XX
XX	WPI; 2001-025250/03.	XX
PT		PT
PT	Nucleic acid encoding a tumor necrosis factor receptor 10, useful in the	PT
PT	diagnosis, treatment or prevention of cancer, autoimmune disorders, and	PT
XX	diseases and disorders associated with apoptosis.	XX
PS		PS
XX	Disclosure; Fig 2; 212pp; English.	XX
CC	The present sequence is given in a specification relating to an isolated	CC
CC	nucleic acid encoding a human tumour necrosis factor receptor TR10. The	CC
CC	TR10 polynucleotide, polypeptide, antibodies, agonists and antagonists	CC
CC	are useful in the diagnosis, treatment or prevention of cancer, such as	CC
CC	breast and ovarian cancer and leukaemia; autoimmune disorders such as	CC
CC	multiple sclerosis, Crohn's disease and graft versus host disease;	CC
CC	diseases associated with increased apoptosis such as AIDS, Alzheimer's	CC
CC	disease and Parkinson's disease; cardiovascular disorders such as limb	CC
CC	ischaemia and congenital heart defects; inflammatory diseases e.g.	CC
CC	allergy; wound healing; disorders associated with neovascularisation,	CC
CC	e.g. diabetic retinopathy; infectious diseases such as viral, bacterial,	CC
CC	fungal and parasitic infections; and neurological diseases such as	CC
CC	amyotrophic lateral sclerosis	CC
SQ		SQ
XX	Sequence 427 AA;	XX
Query Match	89.7%; Score 1244; DB 4; Length 427;	
Best Local Similarity	90.7%; Pred. No. 2,6e-88;	
Matches 225; Conservative	6; Mismatches 17; Indels 0; Gaps 0;	
OY	4 AGAAGCANDRLRLILLILGVSSGAKETCSGLYTHSGECCKACNIGEGVAQCAGANQT 63	OY
DB	3 AGAAGRAMDGPRLILLILGVSLGAKAEAPFTGLYTHSGCCCKACNIGEGVAQCAGANQT 62	DB
OY	64 VCEPCILNMTFSPDVASATEPCPKPTECTCLGQSMGAPCEVADDAYCAVCAYGYODETGHC 123	OY
DB	63 VCEPCILDSVTFSPDVASATEPCPKPTECEVGQSMGAPCEVADDAYCAVCAYGYODETGORC 122	DB
OY	124 EACGVCVGGSGLVFSCODKONTVCEECPEEGTISDEAHVNDPLCPYCEPTERDLRECTP 183	OY
DB	123 EACGVCVGGSGLVFSCODKONTVCEECPEEGTISDEAHVNDPLCPYCEPTERDLRECTP 182	DB
OY	184 WADACEEIEGRWIPRSTPEEGSHSTAPSTQEPREVPPEODLVPSVDAMVTVVSSQPV 243	OY
DB	183 WADACEEIEGRWTRSTPEEGSHSTAPSTQEPREVPPEODLVSTAGVTVTVVSSQPV 242	DB
OY	244 VTRGTTDN 251	OY
DB	243 VTRGTTDN 250	DB
RESULT 8		
AAB36699	ID AAB36699 standard; protein: 427 AA.	
AC	AAB36699;	
XX	15-MAR-2001 (first entry)	
DE	Human tumour necrosis factor receptor NGFR protein SBQ ID NO:5.	
XX	Human; tumour necrosis factor receptor 5; TR1D; TNFR-5; TR5; nontropic;	
KM	TRAIL receptor without intracellular domain; diagnosis; cytostatic;	
KM	tumour necrosis factor related apoptosis inducing ligand; vasotropic;	
KM	immunopreventive; neuroprotective; antiviral; antiinflammatory;	

KM anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
 KM gene therapy; resection; graft versus host disease; tumour; cancer;
 KM apoptotic cell death related disease; autoimmune disorder;
 KM cardiovascular disorder; viral infection.
 OS Homo sapiens.
 XX WO200071150-A1.
 PN 30-NOV-2000.
 PD 18-MAY-2000; 2000WO-US013515.
 PF 20-MAY-1999; 99US-0135164P.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PA Wei Y, Ruben SM, Gentz RL, Ni J.
 PI WPI, 2001-041051/05.
 DR Nucleic acid encoding a TRID polypeptide, also referred to as tumour
 XX necrosis factor receptor 5, useful in the diagnosis, treatment or
 XX prevention of cancer, autoimmune disorders and viral infection.
 PS Disclosure; Fig 2; 285pp; English.
 XX The present invention describes the human TRID protein (tumour necrosis
 CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
 CC intracellular domain, also referred to as tumour necrosis factor receptor
 CC 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, necrotic,
 CC neuroprotective, antiviral, antiinflammatory, anticonvulsant,
 CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
 CC activities, and can be used in gene therapy. The TRID polynucleotides are
 CC useful for detecting complementary polynucleotides. TRID proteins and
 CC polynucleotides are useful in the treatment of tumours, resistance to
 CC parasite, bacteria and viruses, resection and graft versus host disease.
 CC They are also useful for inducing proliferation of T-cells, endothelial
 CC cells and certain haematopoietic cells, to regulate antiviral responses
 CC and to prevent certain autoimmune diseases after stimulation of TRID by
 CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID
 CC polypeptides are useful for treating and/or preventing diseases
 CC associated with increased or decreased apoptotic cell death. The TRID
 CC polynucleotides, proteins, antibodies, agonists and antagonists are
 CC useful in the diagnosis, treatment or prevention of: (a) cancer; (b)
 CC autoimmune disorders; (c) diseases associated with increased apoptosis;
 CC (d) cardiovascular disorders; and (e) viral infection. The present
 CC sequence represents a tumour necrosis factor receptor used in comparison
 CC with TRID in the exemplification of the present invention
 SQ Sequence 427 AA;
 Query Match 89.7%; Score 1244; DB 4; Length 427;
 Best Local Similarity 90.7%; Pred. No. 2.6e-88;
 Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;
 QY 4 AGAAGSAMDRLRLILLILGVSSGAKETCTGLYTHSGECKACNLGEGVAPCCANOT 63
 DB 3 AGATGRAMDGRLLILLILGVSLGAKAECPTGLYTHSGECKACNLGEGVAPCCANOT 62
 QY 64 VCEPCLDNTFSDVSVATPECKPCTECTGLQMSAPCEADAVRCAGVYODEBTGHC 123
 DB 63 VCEPCLDNTFSDVSVATPECKPCTECTGLQMSAPCEADAVRCAGVYODEBTGHC 122
 QY 124 EACSVCEVSGLVFSCODKONTVCECEPEGTYSDEANHYDPCLPCTVCEDETEROURECTP 183
 DB 123 EACRVCBAGSLVFSODKONTVCECEPEGTYSDEANHYDPCLPCTVCEDETEROURECTP 182
 QY 184 WAAABCEETFGRWIPSTPEGSSTAPSTOBEVPEBODIVPSTADVTTVMSSOPV 243
 DB 183 WAAABCEETFGRWIPSTPEGSSTAPSTOBEVPEBODIVPSTADVTTVMSSOPV 242
 QY 244 VTRGTTDN 251

DB 243 VTRGTTDN 250
 RESULT 9
 ID AAE21670
 XX AAE21670 standard; protein; 427 AA.
 AC AAE21670;
 XX 16-JUL-2002 (first entry)
 DT 16-JUL-2002 (first entry)
 DE Human neurotrophic receptor (p75NTR) protein.
 XX Human, diabetic neuropathy; therapy; neurotrophic receptor; p75NTR;
 KM drug screening; receptor.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..28
 FT /label= Signal_peptide
 FT Protein 29..427
 FT /label= Human_mature_p75NTR
 XX WO200218955-A1.
 XX 07-MAR-2002.
 XX 29-AUG-2001; 2001WO-GB003859.
 XX 01-SEP-2000; 2000GB-00021609.
 XX (UYMA-) UNIV VICTORIA MANCHESTER.
 PA Tomlinson DR;
 XX WPI; 2002-329796/36.
 DR Detecting neuropathy, evaluating effect/efficacy of a drug for treating
 XX neuropathy or screening compounds to assess their side effects causing
 FT neuropathy, by detecting 75 kDa Neurotrophic Receptor in patient sample.
 PS Disclosure; Fig 1; 33pp; English.
 XX The invention relates to an in vitro test for neuropathy, for evaluating
 CC whether a subject will benefit from a putative drug for treating
 CC neuropathy. The method comprising detecting for the presence of a 75 kDa
 CC neurotrophic receptor (p75NTR) in a body fluid sample. The invention is
 CC used for diagnosing neuropathy, particularly diabetic neuropathy, for
 CC screening the efficacy of a putative drug for treating neuropathy, for
 CC evaluating whether or not a subject will benefit from a putative drug for
 CC treating neuropathy, for screening a compound to assess whether or not a
 CC compound causes neuropathy, monitoring the health status of a subject
 CC with or at risk of developing neuropathy and testing whether or not a
 CC subject is complying with therapeutic regime for treating diabetes. The
 CC method is also useful for making a detailed analysis such as a clinical
 CC trial of a drug targeted at diabetic neuropathy. The present sequence is
 CC human p75NTR protein
 SQ Sequence 427 AA;
 Query Match 89.7%; Score 1244; DB 5; Length 427;
 Best Local Similarity 90.7%; Pred. No. 2.6e-88;
 Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;
 QY 4 AGAAGSAMDRLRLILLILGVSSGAKETCTGLYTHSGECKACNLGEGVAPCCANOT 63
 DB 3 AGATGRAMDGRLLILLILGVSLGAKAECPTGLYTHSGECKACNLGEGVAPCCANOT 62
 QY 64 VCEPCLDNTFSDVSVATPECKPCTECTGLQMSAPCEADAVRCAGVYODEBTGHC 123
 DB 63 VCEPCLDNTFSDVSVATPECKPCTECTGLQMSAPCEADAVRCAGVYODEBTGHC 122

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: March 12, 2004, 16:28:38 ; Search time 22 seconds
(without alignments)
589.005 Million cell updates/sec

Title: US-09-821-831-4
Perfect score: 1387
Sequence: 1 MRRAGACSMRDLRLILLI.....MTTWGSSQPVTRGTTDN 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1387	100.0	425	US-09-748-537-14	Sequence 14, Appl
2	1244	89.7	427	US-09-086-483A-4	Sequence 4, Appl
3	1244	89.7	427	US-09-041-886-2	Sequence 2, Appl
4	1244	89.7	427	US-09-006-353A-5	Sequence 5, Appl
5	1244	89.7	427	US-09-573-986-5	Sequence 5, Appl
6	1244	89.7	427	US-09-580-212-4	Sequence 4, Appl
7	1244	89.7	427	US-09-769-402-4	Sequence 4, Appl
8	1244	89.7	427	US-09-748-537-13	Sequence 13, Appl
9	1244	89.7	427	US-09-527-236A-4	Sequence 4, Appl
10	1244	89.7	427	US-09-756-854-4	Sequence 4, Appl
11	1133	81.7	224	US-08-974-022-50	Sequence 50, Appl
12	1133	81.7	224	US-08-795-445A-50	Sequence 50, Appl
13	1133	81.7	224	US-08-795-447A-50	Sequence 50, Appl
14	1133	81.7	224	US-08-974-186-50	Sequence 50, Appl
15	1133	81.7	224	US-08-785-446B-50	Sequence 50, Appl
16	1133	81.7	224	US-08-706-945D-137	Sequence 137, Appl
17	1133	81.7	224	US-08-577-788C-51	Sequence 51, Appl
18	891	64.2	159	US-08-232-087A-11	Sequence 11, Appl
19	866	62.4	159	US-08-828-683A-16	Sequence 16, Appl
20	858	61.9	159	US-08-219-237B-6	Sequence 6, Appl
21	858	61.9	159	US-08-468-560C-6	Sequence 6, Appl
22	851	61.4	159	US-08-477-347-15	Sequence 15, Appl
23	851	61.4	159	US-08-476-862-6	Sequence 6, Appl
24	851	61.4	159	US-09-800-909-6	Sequence 6, Appl
25	851	61.4	159	US-09-800-908-15	Sequence 15, Appl
26	402	29.0	76	US-08-866-545-4	Sequence 4, Appl
27	402	29.0	76	US-09-627-775-4	Sequence 4, Appl

28	329	23.7	58	3	US-08-904-446A-15	Sequence 15, Appl
29	307	22.1	58	3	US-08-904-446A-14	Sequence 14, Appl
30	270	19.5	58	3	US-08-904-446A-16	Sequence 16, Appl
31	251	18.1	42	1	US-08-050-319B-42	Sequence 42, Appl
32	251	18.1	42	1	US-08-465-982-42	Sequence 42, Appl
33	233	16.8	42	1	US-08-050-319B-33	Sequence 33, Appl
34	233	16.8	42	1	US-08-465-982-33	Sequence 33, Appl
35	231	16.7	40	1	US-08-050-319B-38	Sequence 38, Appl
36	231	16.7	40	1	US-08-465-982-38	Sequence 38, Appl
37	216.5	15.6	277	2	US-08-469-633A-4	Sequence 4, Appl
38	214	15.4	277	2	US-08-147-784-2	Sequence 2, Appl
39	214	15.4	277	3	US-08-195-967-2	Sequence 2, Appl
40	214	15.4	277	3	US-09-006-353A-12	Sequence 12, Appl
41	214	15.4	277	3	US-08-472-940-2	Sequence 2, Appl
42	214	15.4	277	4	US-09-573-986-12	Sequence 12, Appl
43	214	15.4	277	4	US-09-880-939-2	Sequence 2, Appl
44	214	15.4	277	4	US-09-804-200-2	Sequence 2, Appl
45	211	15.2	419	3	US-08-509-024-7	Sequence 7, Appl

ALIGNMENTS

```
RESULT 1
US-09-748-537-14
Sequence 14, Application US/09748537
Patent No. 6680167
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THERE
FILE REFERENCE: 07334-316001
CURRENT FILING DATE: 2000-12-26
CURRENT APPLICATION NUMBER: US/09/748,537
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 425
TYPE: PRT
ORGANISM: Rattus rattus
US-09-748-537-14

Query Match 100.0%; Score 1387; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 3.6e-113;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRAGACSMRDLRLILLIIGVSSGAKETCTGLYTHSGGCCACNLGEGVAQPCGA 60
DB 1 MRRAGACSMRDLRLILLIIGVSSGAKETCTGLYTHSGGCCACNLGEGVAQPCGA 60

QY 61 NOTVEPCLDNTTSEDVVSATBPCKPCTECUGLQMSAPCYEADAVRCRAGYQDEBT 120
DB 61 NOTVEPCLDNTTSEDVVSATBPCKPCTECUGLQMSAPCYEADAVRCRAGYQDEBT 120

QY 121 GHEACSVCEVSGVFCSCODKONTVCCEPEGTSDANHYDPCLPCTVCEDETRQURE 180
DB 121 GHEACSVCEVSGVFCSCODKONTVCCEPEGTSDANHYDPCLPCTVCEDETRQURE 180

QY 181 CTPMADAECEBIPEGWIPRSTPPGSDSTAPSTQEPFVPPEDLVFSTVADMVTTWSS 240
DB 181 CTPMADAECEBIPEGWIPRSTPPGSDSTAPSTQEPFVPPEDLVFSTVADMVTTWSS 240

QY 241 QPVVTRGTTDN 251
DB 241 QPVVTRGTTDN 251

RESULT 2
US-09-086-483A-4
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Sequence 4, Application US/09086483A
Patent No. 6214580
GENERAL INFORMATION:
APPLICANT: NI, et al.
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,483A
FILING DATE: May-29-98
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/050,936
FILING DATE: May-30-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/069,112
FILING DATE: Dec-9-97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF379
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-086-483A-4

Query Match 89.7%; Score 1244; DB 3; Length 427;
Best Local Similarity 90.7%; Pred. No. 1.1e-100;
Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 4 AGAAGSAMDRLRLILLILGVSSGGAKETCTGLYTHSGECCKACNLGEGVAOPCGANOT 63
DB 3 AGATGRAMDPRILLILLILGVSSGGAKETCTGLYTHSGECCKACNLGEGVAOPCGANOT 62
QY 64 VCEPCLDNVTFPSDVVSATPECKPCTECLGLQSMAPCEVADAVCRCAVGYODEETGHC 123
DB 63 VCEPCLDSVTFPSDVVSATPECKPCTECLGLQSMAPCEVADAVCRCAVGYODEETGHC 122
QY 124 EACSVCEAGSLVSCODKONTVCEBCEGTYSDENAHVDPCLPCTVCEDETERQLRECTP 183
DB 123 EACRVCEAGSLVSCODKONTVCEBCEGTYSDENAHVDPCLPCTVCEDETERQLRECTR 182
QY 184 WADACEEIPGRWIPRSTPEPGSDSTAPSTOEPEVPEPDVLVSTVADMTTWGSSQPV 243
DB 183 WADACEEIPGRWITRSTPEPGSDSTAPSTOEPEVPEPDVLVSTVADMTTWGSSQPV 242
QY 244 VTRGTTDN 251
DB 243 VTRGTTDN 250

RESULT 3
US-09-041-886-2

Sequence 2, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
TITLE OF INVENTION: Rabizaden, Sharioz
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-041-886-2

Query Match 89.7%; Score 1244; DB 3; Length 427;
Best Local Similarity 90.7%; Pred. No. 1.1e-100;
Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 4 AGAAGSAMDRLRLILLILGVSSGGAKETCTGLYTHSGECCKACNLGEGVAOPCGANOT 63
DB 3 AGATGRAMDPRILLILLILGVSSGGAKETCTGLYTHSGECCKACNLGEGVAOPCGANOT 62
QY 64 VCEPCLDNVTFPSDVVSATPECKPCTECLGLQSMAPCEVADAVCRCAVGYODEETGHC 123
DB 63 VCEPCLDSVTFPSDVVSATPECKPCTECLGLQSMAPCEVADAVCRCAVGYODEETGHC 122
QY 124 EACSVCEAGSLVSCODKONTVCEBCEGTYSDENAHVDPCLPCTVCEDETERQLRECTP 183
DB 123 EACRVCEAGSLVSCODKONTVCEBCEGTYSDENAHVDPCLPCTVCEDETERQLRECTR 182
QY 184 WADACEEIPGRWIPRSTPEPGSDSTAPSTOEPEVPEPDVLVSTVADMTTWGSSQPV 243
DB 183 WADACEEIPGRWITRSTPEPGSDSTAPSTOEPEVPEPDVLVSTVADMTTWGSSQPV 242
QY 244 VTRGTTDN 251
DB 243 VTRGTTDN 250

RESULT 4
US-09-006-353A-5
Sequence 5, Application US/09006353A
Patent No. 6261801
GENERAL INFORMATION:
APPLICANT: MEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN


```

; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-006-353A-5

Query Match      89.7%; Score 1244; DB 3; Length 427;
Best Local Similarity 90.7%; Pred. No. 1.1e-100;
Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 4 AGAAGCANDRLRLILLILIGVSSGAKETCTGLYTHSGECKACNLGEGVAGPCGANOT 63
DB 3 AGATGRAMDGPRLILLILIGVSLGAKKACPTGLYTHSGECKACNLGEGVAGPCGANOT 62
QY 64 VCEPCLDNVTFSFSDVVSATPEPCPCTECLGLQSMSPACVEADDAVRCRCAVGYQDEETGHC 123
DB 63 VCEPCLDNVTFSFSDVVSATPEPCPCTECLGLQSMSPACVEADDAVRCRCAVGYQDEETGHC 122
QY 124 EACSVCEVSGSLVFSQCKQNTVCECEPCEGTYSDANHVDPCLPCTVCEDETERQLRECTP 183
DB 123 EACRVCEAGSGLVFSCQCKQNTVCECEPCEGTYSDANHVDPCLPCTVCEDETERQLRECTP 182
QY 184 WADACEEIPGRWIPRSTPEPGSDSTAPSTQEPVEVPPEODLVPSTVADMTVTWSSQPV 243
DB 183 WADACEEIPGRWIPRSTPEPGSDSTAPSTQEPVEVPPEODLVPSTVADMTVTWSSQPV 242
QY 244 VTRGTTDN 251
DB 243 VTRGTTDN 250

RESULT 5
US-09-573-986-5
; Sequence 5, Application US/09573986
; Patent No. 6455040
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reinex
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.128004
; CURRENT APPLICATION NUMBER: US/09/573,986
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27

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; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-573-986-5

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Best Local Similarity 90.7%; Pred. No. 1.1e-100;
Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

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DB 123 EACRVCEAGSGLVFSCQCKQNTVCECEPCEGTYSDANHVDPCLPCTVCEDETERQLRECTP 182
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DB 183 WADACEEIPGRWIPRSTPEPGSDSTAPSTQEPVEVPPEODLVPSTVADMTVTWSSQPV 242
QY 244 VTRGTTDN 251
DB 243 VTRGTTDN 250

RESULT 6
US-09-580-212-4
; Sequence 4, Application US/09580212
; Patent No. 6506569
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR10
; FILE REFERENCE: PF379P1
; CURRENT APPLICATION NUMBER: US/09/580,212
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/136,786
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,563
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/144,023
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-580-212-4

Query Match      89.7%; Score 1244; DB 4; Length 427;
Best Local Similarity 90.7%; Pred. No. 1.1e-100;
Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

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DB 3 AGATGRAMDGPRLILLILIGVSLGAKKACPTGLYTHSGECKACNLGEGVAGPCGANOT 62
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DB 63 VCEPCLDNVTFSFSDVVSATPEPCPCTECLGLQSMSPACVEADDAVRCRCAVGYQDEETGHC 122
QY 124 EACSVCEVSGSLVFSQCKQNTVCECEPCEGTYSDANHVDPCLPCTVCEDETERQLRECTP 183
DB 123 EACRVCEAGSGLVFSCQCKQNTVCECEPCEGTYSDANHVDPCLPCTVCEDETERQLRECTP 182
QY 184 WADACEEIPGRWIPRSTPEPGSDSTAPSTQEPVEVPPEODLVPSTVADMTVTWSSQPV 243
DB 183 WADACEEIPGRWIPRSTPEPGSDSTAPSTQEPVEVPPEODLVPSTVADMTVTWSSQPV 242

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Db 183 WADACEEELIPGRWITRSTPEGSDSTAPSTQEPPEAPPEODLIASIVAGVTTWSSQPV 242
QY 244 VTRGTTDN 251
Db 243 VTRGTTDN 250

RESULT 7

US-09-769-402-4
Sequence 4, Application US/09769402
Patent No. 6607726
GENERAL INFORMATION:
APPLICANT: NI, et al.
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769,402
FILING DATE: 26-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/086,483
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/069,112
FILING DATE: Dec-9-97
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF379
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-769-402-4

Query Match 89.7%; Score 1244; DB 4; Length 427;
Best Local Similarity 90.7%; Pred. No. 1.1e-100;
Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 4 AGAAGCAMPDRLLRLIIIGVSSGAKETCTGLYTHSGECCACNLGEGVAPCGANOT 63
Db 3 AGATGRAMDGPRLIIIGVSLGAKAEPFTGLYTHSGECCACNLGEGVAPCGANOT 62
QY 64 VCEPCLDNVTFSVDVSAATEPCCKTECLGLOSMAFCVADDAVGCAGVYQDEETGHC 123
Db 63 VCEPCLDVTFSDVVSATEPCCKTECLGLOSMAFCVADDAVGCAGVYQDEETGHC 122
QY 124 EASVCEVSGGLVFSQDKONTVCCECPGEGTSDANHVDPCLPCTVCEDTERQLRECTP 183
Db 123 EACVCEVSGGLVFSQDKONTVCCECPGEGTSDANHVDPCLPCTVCEDTERQLRECTP 182
QY 184 WADACEEELIPGRWITRSTPEGSDSTAPSTQEPPEAPPEODLIASIVAGVTTWSSQPV 243
Db 183 WADACEEELIPGRWITRSTPEGSDSTAPSTQEPPEAPPEODLIASIVAGVTTWSSQPV 242

QY 244 VTRGTTDN 251
Db 243 VTRGTTDN 250

RESULT 8

US-09-748-537-13
Sequence 13, Application US/09748537
Patent No. 6680167
GENERAL INFORMATION:
APPLICANT: Bertin, John
APPLICANT: Chao, Moses V.
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
FILE REFERENCE: 07334-316001
CURRENT APPLICATION NUMBER: US/09/748,537
CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 427
TYPE: PRT
ORGANISM: Homo sapiens
US-09-748-537-13

Query Match 89.7%; Score 1244; DB 4; Length 427;
Best Local Similarity 90.7%; Pred. No. 1.1e-100;
Matches 225; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 4 AGAAGCAMPDRLLRLIIIGVSSGAKETCTGLYTHSGECCACNLGEGVAPCGANOT 63
Db 3 AGATGRAMDGPRLIIIGVSLGAKAEPFTGLYTHSGECCACNLGEGVAPCGANOT 62
QY 64 VCEPCLDNVTFSVDVSAATEPCCKTECLGLOSMAFCVADDAVGCAGVYQDEETGHC 123
Db 63 VCEPCLDVTFSDVVSATEPCCKTECLGLOSMAFCVADDAVGCAGVYQDEETGHC 122
QY 124 EASVCEVSGGLVFSQDKONTVCCECPGEGTSDANHVDPCLPCTVCEDTERQLRECTP 183
Db 123 EACVCEVSGGLVFSQDKONTVCCECPGEGTSDANHVDPCLPCTVCEDTERQLRECTP 182
QY 184 WADACEEELIPGRWITRSTPEGSDSTAPSTQEPPEAPPEODLIASIVAGVTTWSSQPV 243
Db 183 WADACEEELIPGRWITRSTPEGSDSTAPSTQEPPEAPPEODLIASIVAGVTTWSSQPV 242
QY 244 VTRGTTDN 251
Db 243 VTRGTTDN 250

RESULT 9

US-09-527-236A-4
Sequence 4, Application US/09527236A
Patent No. 6358508
GENERAL INFORMATION:
APPLICANT: NI, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Fan, Ping
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PF375P1
CURRENT APPLICATION NUMBER: US/09/527,236A
CURRENT FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/052,991
PRIOR FILING DATE: 1997-06-11
PRIOR APPLICATION NUMBER: 09/095,094
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/126,019
PRIOR FILING DATE: 1999-03-24

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 12, 2004, 16:29:08 ; Search time 35 Seconds
(without alignments)
1514.271 Million cell updates/sec

Title: US-09-821-831-4

Perfect score: 1387
Sequence: 1 MRRAGAACAMDRRLRLLL.....MTTWGSGQPVYTRGTEN 251

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 21153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1387	100.0	425	9	US-09-748-537-4
3	1387	100.0	425	9	US-09-821-831-2
4	1244	89.7	427	8	US-08-681-219-26
5	1244	89.7	427	9	US-09-826-212-5
6	1244	89.7	427	9	US-09-748-537-13
7	1244	89.7	427	9	US-09-935-727-7
8	1244	89.7	427	11	US-09-230-111C-24
9	1244	89.7	427	14	US-10-155-886-5
10	1244	89.7	427	14	US-10-186-643-5
11	1244	89.7	427	14	US-10-092-138-24
12	1244	89.7	427	14	US-10-280-047-4
13	1244	89.7	427	15	US-10-418-242-7
14	1244	89.7	455	9	US-09-756-854-4
15	1244	89.7	455	13	US-10-041-574-4

16	1133	81.7	224	11	US-09-405-032-134	Sequence 134, App
17	866	62.4	159	13	US-10-112-793-16	Sequence 16, Appl
18	858	61.9	159	9	US-09-884-987-6	Sequence 6, Appl1
19	851	61.4	159	9	US-09-800-908-6	Sequence 6, Appl1
20	851	61.4	159	9	US-09-800-908-15	Sequence 15, Appl1
21	851	61.4	159	15	US-10-423-927-6	Sequence 6, Appl1
22	214	15.4	274	9	US-09-836-607-3	Sequence 3, Appl1
23	214	15.4	274	10	US-09-421-112-3	Sequence 3, Appl1
24	214	15.4	277	9	US-09-825-211-12	Sequence 12, Appl1
25	214	15.4	277	9	US-09-852-845-2	Sequence 2, Appl1
26	214	15.4	277	9	US-09-804-200-2	Sequence 2, Appl1
27	214	15.4	277	9	US-09-800-939-2	Sequence 2, Appl1
28	214	15.4	277	9	US-09-768-779A-5	Sequence 5, Appl1
29	214	15.4	277	9	US-09-935-727-14	Sequence 14, Appl1
30	214	15.4	277	14	US-10-140-164-6	Sequence 6, Appl1
31	214	15.4	277	14	US-10-046-433-3	Sequence 3, Appl1
32	214	15.4	277	14	US-10-291-480-5	Sequence 14, Appl1
33	214	15.4	277	14	US-10-186-613-12	Sequence 12, Appl1
34	214	15.4	277	14	US-10-207-655-158	Sequence 158, App
35	214	15.4	277	14	US-10-073-333A-6	Sequence 6, Appl1
36	214	15.4	277	14	US-10-326-929-2	Sequence 2, Appl1
37	214	15.4	277	15	US-10-323-274C-2	Sequence 2, Appl1
38	214	15.4	277	15	US-10-418-242-14	Sequence 14, Appl1
39	211	15.2	419	9	US-09-924-231-7	Sequence 7, Appl1
40	210	15.1	276	15	US-10-369-300-4	Sequence 4, Appl1
41	208	15.0	197	9	US-09-934-289A-18	Sequence 18, Appl1
42	207	14.9	444	14	US-10-363-447-2	Sequence 2, Appl1
43	205.5	14.8	909	14	US-10-226-296-4	Sequence 4, Appl1
44	205.5	14.8	909	14	US-10-226-318-4	Sequence 4, Appl1
45	204.5	14.7	336	9	US-09-756-166-8	Sequence 8, Appl1

ALIGNMENTS

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RESULT 1
US-09-821-831-4
Sequence 4, Application US/09821831
Patent No. US20020137188A1
GENERAL INFORMATION:
APPLICANT: Bartlett, Perry Francis
APPLICANT: Coulson, Elizabeth Jane
APPLICANT: Fieldew, Katrina
APPLICANT: Baca, Manuel
APPLICANT: Kilpatrick, Trevor
APPLICANT: Surindat, Cheema
TITLE OF INVENTION: Method of Modulating Cell Survival and
FILE REFERENCE: 3206.1001-000
CURRENT APPLICATION NUMBER: US/09/821,831
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: PCT/AU99/00860
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: AU PQ0701
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: AU PP6351
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: AU PP6353
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FaSTSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 251
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Deduced amino acid sequence
US-09-821-831-4
Query Match 100.0% Score 1387; DB 9; Length 251;
Best Local Similarity 100.0%; Pred.No. 1.3e-107;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MRAGAACSAMDRLRLILLILGVSSGAGKTCSTGLYTHSGECCCKACNLGEGVAQPCGA 60
DB 1 MRAGAACSAMDRLRLILLILGVSSGAGKTCSTGLYTHSGECCCKACNLGEGVAQPCGA 60
QY 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQSMAPCEVADDAVCRCAVGYODEET 120
DB 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQSMAPCEVADDAVCRCAVGYODEET 120
QY 121 GHGACGVCVSGSLVFSQCDKONTVCECEPCEGTYSDEAHNVDPCLPCTVCEDETERQLRE 180
DB 121 GHGACGVCVSGSLVFSQCDKONTVCECEPCEGTYSDEAHNVDPCLPCTVCEDETERQLRE 180
QY 181 CTPWADACEEIPGRWIPRSTPPEGSSTAPSTQEPPEVPEODLVSTVADMTVTWSS 240
DB 181 CTPWADACEEIPGRWIPRSTPPEGSSTAPSTQEPPEVPEODLVSTVADMTVTWSS 240
QY 241 QPVTRGTIDN 251
DB 241 QPVTRGTIDN 251

RESULT 2

US-09-748-537-14
Sequence 14, Application US/09748537
Patent No. US20020061833A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
APPLICANT: Chao, Moses V.
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILIE AND USES THERE
FILE REFERENCE: 07334-316001
CURRENT APPLICATION NUMBER: US/09/748,537
PRIOR FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 425
TYPE: PRT
ORGANISM: Rattus rattus
US-09-748-537-14

Query Match 100.0%; Score 1387; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 2.3e-107;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MRAGAACSAMDRLRLILLILGVSSGAGKTCSTGLYTHSGECCCKACNLGEGVAQPCGA 60
QY 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQSMAPCEVADDAVCRCAVGYODEET 120
DB 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQSMAPCEVADDAVCRCAVGYODEET 120
QY 121 GHGACGVCVSGSLVFSQCDKONTVCECEPCEGTYSDEAHNVDPCLPCTVCEDETERQLRE 180
DB 121 GHGACGVCVSGSLVFSQCDKONTVCECEPCEGTYSDEAHNVDPCLPCTVCEDETERQLRE 180
QY 181 CTPWADACEEIPGRWIPRSTPPEGSSTAPSTQEPPEVPEODLVSTVADMTVTWSS 240
DB 181 CTPWADACEEIPGRWIPRSTPPEGSSTAPSTQEPPEVPEODLVSTVADMTVTWSS 240
QY 241 QPVTRGTIDN 251
DB 241 QPVTRGTIDN 251

RESULT 3
US-09-821-831-2
Sequence 2, Application US/09821831
Patent No. US20020137188A1

GENERAL INFORMATION:
APPLICANT: Bartlett, Perry Francis
APPLICANT: Coulson, Elizabeth Jane
APPLICANT: Fielder, Katrina
APPLICANT: Baca, Manuel
APPLICANT: Kilpatrick, Trevor
APPLICANT: Surindar, Cheema
TITLE OF INVENTION: Method of Modulating Cell Survival and
FILE REFERENCE: 3206-1001-000
CURRENT APPLICATION NUMBER: US/09/821,831
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: PCT/AU99/00860
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: AU PQ0701
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: AU PE6351
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: AU PE6353
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 425
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Deduced amino acid sequence
US-09-821-831-2

Query Match 100.0%; Score 1387; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 2.3e-107;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MRAGAACSAMDRLRLILLILGVSSGAGKTCSTGLYTHSGECCCKACNLGEGVAQPCGA 60
QY 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQSMAPCEVADDAVCRCAVGYODEET 120
DB 61 NOTVCEPCLDNVTFSDVVSATPECKPCTECLGLQSMAPCEVADDAVCRCAVGYODEET 120
QY 121 GHGACGVCVSGSLVFSQCDKONTVCECEPCEGTYSDEAHNVDPCLPCTVCEDETERQLRE 180
DB 121 GHGACGVCVSGSLVFSQCDKONTVCECEPCEGTYSDEAHNVDPCLPCTVCEDETERQLRE 180
QY 181 CTPWADACEEIPGRWIPRSTPPEGSSTAPSTQEPPEVPEODLVSTVADMTVTWSS 240
DB 181 CTPWADACEEIPGRWIPRSTPPEGSSTAPSTQEPPEVPEODLVSTVADMTVTWSS 240
QY 241 QPVTRGTIDN 251
DB 241 QPVTRGTIDN 251

RESULT 4

US-08-681-219-26
Sequence 26, Application US/08681219
Patent No. US20020058607A1
GENERAL INFORMATION:
APPLICANT: Takaki, Sato and Junn Yanagisawa
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GIGF
TITLE OF INVENTION: (PDZ/DHR) DOMAIN AND USES THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: March 12, 2004, 16:27:22 ; Search time 18 seconds

(without alignments)
726.089 Million cell updates/sec

Title: US-09-821-831-4

Perfect score: 1387
Sequence: 1 MRRAGAGACGANDRLRLLL.....MTTWGSSGPVTRGTTDN 251

Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	215.5	15.5	461	TR1A_RAT	P22934 ratu
6	214	15.4	277	TR1A_HUMAN	P43489 homo sapien
7	211	15.2	204	TR26_MOUSE	P83626 mus musculu
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9	202	14.6	289	TR15_MOUSE	P27512 mus musculu
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13	194	14.0	401	TR1B_MOUSE	O06712 mus musculu
14	193.5	14.0	326	VT2_MXVXL	P23825 MYXOMA VIRU
15	191.5	13.8	259	TR10C_HUMAN	O14798 h tumor nec
16	189.5	13.7	271	TR14_RAT	P15725 ratu
17	189.5	13.7	401	TR1B_HUMAN	O00300 homo sapien
18	188	13.6	471	TR1A_BOVIN	O15131 bos taurus
19	186.5	13.4	272	TR1A_MOUSE	P50284 mus musculu
20	183	13.2	415	TR1A_MOUSE	O75509 homo sapien
21	181	13.0	655	TR21_HUMAN	P25119 mus musculu
22	180.5	13.0	474	TR1B_MOUSE	Q960W1 mus musculu
23	176	12.7	655	TR21_MOUSE	Q960W1 mus musculu
24	175.5	12.7	277	TR15_HUMAN	P25942 homo sapien
25	175	12.6	198	TR22_MOUSE	Q960W1 mus musculu
26	175	12.6	435	TR1A_HUMAN	P36941 homo sapien
27	173	12.5	401	TR1B_RAT	O08727 ratu
28	171.5	12.4	3075	TR1A_HUMAN	Q960W1 mus musculu
29	171	12.3	176	TR23_MOUSE	Q960W1 mus musculu
30	171	12.3	461	TR1A_PIG	P50555 sus scrofa
31	170.5	12.3	461	TR1B_HUMAN	P20333 homo sapien
32	170.5	12.3	616	TR11_HUMAN	Q960W1 mus musculu
33	168	12.1	300	TR16_HUMAN	O95407 homo sapien

34	163	11.8	324	1	TR16_RAT	Q63199 ratu
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36	156	11.2	335	1	TR16_HUMAN	P25445 homo sapien
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38	154.5	11.1	327	1	TR16_MOUSE	P25446 mus musculu
39	154	11.1	332	1	TR16_PIG	O77736 sus scrofa
40	154	11.1	468	1	TR10A_HUMAN	O00220 homo sapien
41	154	11.1	1816	1	TR1A_HUMAN	Q16363 homo sapien
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45	149	10.7	269	1	TR15_BOVIN	Q28203 bos taurus

ALIGNMENTS

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ID TR16_RAT STANDARD; PRT; 425 AA.
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DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 16 precursor (low-affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
DE (p75 ICD) (low affinity neurotrophin receptor p75NTR)
GN NGFR OR TNFRSF16.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=67115859; PubMed=3027580;
RA Radeke M.J., Misko T.P., Hsu C., Herzberg L.A., Shooter E.M.;
RT "Gene transfer and molecular cloning of the rat nerve growth factor receptor.";
RL Nature 325:593-597(1987).
RN [2]
RP SEQUENCE OF 1-22 FROM N.A.
RX TISSUE=Liver;
RA MEDLINE=93077038; PubMed=1446821;
RA Metels M., Timmusk T., Allkneets R., Saarna M., Persson H.;
RT "Regulatory elements and transcriptional regulation by testosterone and retinoic acid of the rat nerve growth factor receptor promoter.";
RL Gene 121:247-254(1992).
RN [3]
RP STRUCTURE BY NMR OF 334-418.
RX MEDLINE=97449145; PubMed=9305641;
RA Liepish E., Illeg L.L., Oetting G., Ibanez C.F.;
RT "NMR structure of the death domain of the p75 neurotrophin receptor.";
RL EMBO J. 16:4999-5005(1997).
CC -1- FUNCTION: low affinity receptor which can bind to NGF, BDNF, NT-3, and NT-4. Can mediate cell survival as well as cell death of neural cells.
CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR associated cell death executor. Interacts with TRAF2, TRAF4, TRAF6 and PRIN3 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: N- and O-glycosylated.
CC -1- PTM: Phosphorylated on serine residues.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -1- SIMILARITY: Contains 1 death domain.
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DR EMBL; X05137; CA28783.1; -
 DR EMBL; X61269; -; NOT_ANNOTATED_CDS.
 DR PIR; A26431; A26431.
 DR PDB; INGR; 29-JUL-97.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS00650; TNFR_NGFR_2; 4.
 DR PROSITE; PS0017; DEATH_DOMAIN; 1.
 DR Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
 Receptor; Phosphorylation; Signal; 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 425
 FT DOMAIN 30 251
 FT TRANSMEM 252 273
 FT DOMAIN 274 425
 FT REPEAT 32 65
 FT REPEAT 67 108
 FT REPEAT 109 147
 FT REPEAT 149 189
 FT DOMAIN 354 419
 FT DOMAIN 198 249
 FT DISULFID 33 44
 FT DISULFID 45 58
 FT DISULFID 48 65
 FT DISULFID 68 84
 FT DISULFID 87 100
 FT DISULFID 90 108
 FT DISULFID 110 123
 FT DISULFID 126 139
 FT DISULFID 129 147
 FT DISULFID 150 165
 FT DISULFID 168 181
 FT DISULFID 171 189
 FT CARBOHYD 61 64
 FT CARBOHYD 71 71
 SQ SEQUENCE 425 AA; 45432 MW; B2E152D94D3827F8 CRC64;
 Query Match 100.0%; Score 1387; DB 1; Length 425;
 Best Local Similarity 100.0%; Pred. No. 7,8e-99;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRRAGAACAMDLRLILLIIGVSGGAKETCSGLYTHSGECCKACNLGAGVAPQCA 60
 DB 1 MRRAGAACAMDLRLILLIIGVSGGAKETCSGLYTHSGECCKACNLGAGVAPQCA 60
 QY 61 NOTVCBPCLDNVPFSDVNSATEBCKPCTECLGLQSWASACVEADPAVCAAGYODEET 120
 DB 61 NOTVCBPCLDNVPFSDVNSATEBCKPCTECLGLQSWASACVEADPAVCAAGYODEET 120
 QY 121 GHCEACVCEVSGGLVFSQCDKONTVCEBCEBGTVDENAHVDPCLPCTVCEDETEROLRE 180
 DB 121 GHCEACVCEVSGGLVFSQCDKONTVCEBCEBGTVDENAHVDPCLPCTVCEDETEROLRE 180
 QY 121 GHCEACVCEVSGGLVFSQCDKONTVCEBCEBGTVDENAHVDPCLPCTVCEDETEROLRE 180
 DB 121 GHCEACVCEVSGGLVFSQCDKONTVCEBCEBGTVDENAHVDPCLPCTVCEDETEROLRE 180
 QY 181 CTFMACAECEIIGRMIPRSTPEGSDDTAPSTQSEVEVEPEODIVSTVADAVTTVMGSS 240
 DB 181 CTFMACAECEIIGRMIPRSTPEGSDDTAPSTQSEVEVEPEODIVSTVADAVTTVMGSS 240
 QY 241 QPVVTRGTDN 251
 DB 241 QPVVTRGTDN 251
 RESULT 2
 ID TR16_MOUSE STANDARD; PRT; 417 AA.
 AC Q920M1;
 DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 16 precursor (low-
 DE affinity nerve growth factor receptor) (NGF receptor) (low affinity
 DE neurotrophin receptor p75NTR).
 GN NGFR OR TNFRSF16.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A.
 RX MEDLINE=99077793; PubMed=9857182;
 RA Tuffreau C., Benejean J., Blondel D., Kieffer B., Flamand A.;
 RT "Low-affinity nerve-growth factor receptor (p75NTR) can serve as a
 RT receptor for rabies virus.";
 RL EMO J. 17:7250-7259(1998).
 CC -1- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3,
 CC AND NT-4. Can mediate cell survival as well as cell death of
 CC neural cells (By similarity). Binds to rabies virus glycoprotein
 CC Gs.
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
 CC associated cell death executor. Interacts with TRAF2, TRAF4,
 CC TRAF6 and TRPM3 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- PTM: Phosphorylated on serine residues (By similarity).
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; AF105292; AAD17943.1; -
 DR HSSP; P07174; INGR.
 DR MSD; MGI:97323; NGfr.
 DR GO; GO:0005035; F:death receptor activity; IDA.
 DR GO; GO:0005035; F:protein binding; IPI.
 DR GO; GO:0007411; P:axon guidance; IMP.
 DR GO; GO:0007417; P:central nervous system development; IMP.
 DR GO; GO:0006917; P:induction of apoptosis; IDA.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS00650; TNFR_NGFR_2; 4.
 DR PROSITE; PS0017; DEATH_DOMAIN; 1.
 DR Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
 DR Receptor; Phosphorylation; Signal; 3D-structure.
 FT SIGNAL 1 21
 FT CHAIN 22 417
 FT DOMAIN 22 246
 FT TRANSMEM 247 265
 FT DOMAIN 266 417
 FT REPEAT 24 57
 FT REPEAT 59 100
 FT REPEAT 101 139
 FT REPEAT 141 181
 FT REPEAT 144 411
 FT DOMAIN 346 411
 FT DOMAIN 190 241
 FT DISULFID 25 36
 FT DISULFID 37 50
 FT DISULFID 57 57
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
 CC associated cell death executor. Interacts with TRAF2, TRAF4,
 CC TRAF6 and TRPM3 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- PTM: Phosphorylated on serine residues (By similarity).
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.
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 CC -----
 DR EMBL; AF105292; AAD17943.1; -
 DR HSSP; P07174; INGR.
 DR MSD; MGI:97323; NGfr.
 DR GO; GO:0005035; F:death receptor activity; IDA.
 DR GO; GO:0005035; F:protein binding; IPI.
 DR GO; GO:0007411; P:axon guidance; IMP.
 DR GO; GO:0007417; P:central nervous system development; IMP.
 DR GO; GO:0006917; P:induction of apoptosis; IDA.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS00650; TNFR_NGFR_2; 4.
 DR PROSITE; PS0017; DEATH_DOMAIN; 1.
 DR Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;
 DR Receptor; Phosphorylation; Signal; 3D-structure.
 FT SIGNAL 1 21
 FT CHAIN 22 417
 FT DOMAIN 22 246
 FT TRANSMEM 247 265
 FT DOMAIN 266 417
 FT REPEAT 24 57
 FT REPEAT 59 100
 FT REPEAT 101 139
 FT REPEAT 141 181
 FT REPEAT 144 411
 FT DOMAIN 346 411
 FT DOMAIN 190 241
 FT DISULFID 25 36
 FT DISULFID 37 50
 FT DISULFID 57 57
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR-
 CC associated cell death executor. Interacts with TRAF2, TRAF4,
 CC TRAF6 and TRPM3 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- PTM: N- and O-glycosylated (By similarity).
 CC -1- PTM: Phosphorylated on serine residues (By similarity).
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.
 CC -----
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 CC -----

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FT DISULFID 60 76 BY SIMILARITY.
FT DISULFID 79 92 BY SIMILARITY.
FT DISULFID 82 100 BY SIMILARITY.
FT DISULFID 102 115 BY SIMILARITY.
FT DISULFID 118 131 BY SIMILARITY.
FT DISULFID 121 139 BY SIMILARITY.
FT DISULFID 142 157 BY SIMILARITY.
FT DISULFID 160 173 BY SIMILARITY.
FT DISULFID 163 181 BY SIMILARITY.
FT CARBOHYD 53 53 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 417 AA; 44666 MW; 5D7A4510DB8AF9B2 CMC64;

Query Match 89.9%; Score 1247; DB 1; Length 417;
Best Local Similarity 92.6%; Pred. No. 3,6e-88;
Matches 225; Conservative 6; Mismatches 10; Indels 2; Gaps 1;

QY 11 MDRLR-LLILLIGVSSGSGAKETGSLTHSGECCKACNLGSGVAPCCANQTVCEPC 68
DB 1 MDRLRLLILLIGVSSGSGAKETGSLTHSGECCKACNLGSGVAPCCANQTVCEPC 60
QY 69 LDNTVPSDVATPECKPCTECLGIQSNAPCEVADAVCAVGYQDEBTGCEACSV 128
DB 61 LDNTVPSDVATPECKPCTECLGIQSNAPCEVADAVCAVGYQDEBTGCEACSV 120
QY 129 CEVSGVLESCODKNTVCECPPEGTYSDEANHTDPCLPCTVCEDTROLRCECPMADAE 188
DB 121 CEVSGVLESCODKNTVCECPPEGTYSDEANHTDPCLPCTVCEDTROLRCECPMADAE 180
QY 189 CEETPGRWIPRSTPEGSSTAPSTOBEVPEODLVPSTVADAVTTVMSSQPVYTRGT 248
DB 181 CEETPGRWIPRSTPEGSSTAPSTOBEVPEODLVPSTVADAVTTVMSSQPVYTRGT 240
QY 249 TDN 251
DB 241 ADN 243

Db
QY 249 TDN 251
DB 241 ADN 243

RESULT 3
TR16 HUMAN STANDARD; PRT; 427 AA.
ID TR16 HUMAN STANDARD; PRT; 427 AA.
AC P08138.
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 16 precursor (low-
DE affinity nerve growth factor receptor) (NGF receptor) (p75-NGFR)
DE (p75 ICD) (Low affinity neurotrophin receptor p75NTR).
GN NGFR OR TNFRSF16.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP MEDLINE=87051725; PubMed=3022937;
RA Johnson D., Lannan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,
RA Botwell M., Chao M.;
RT "Expression and structure of the human NGF receptor.";
RL Cell 47:545-554(1986).
RN [2]
RP SEQUENCE FROM N.A.
RP TISSUE=Brain;
RA MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schiezel T.E.,
RA Brownstein M.J., Ueda T.B., Tomihata S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratnam P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

```


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CM protein - protein search, using sw model

Run on: March 12, 2004, 16:27:22 / Search time 45 Seconds

(without alignments)
1759.890 Million cell updates/sec

Title: US-09-821-831-4

Perfect score: 1367
Sequence: 1 MRACAGACASMDRLRLDLLL.....MTTWGSSQPVVTRGTTDN 251

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1297	93.5	427	11	Q8CFT3 Q8CFT3 mus musculus
2	1247	89.9	417	11	Q8BYX1 Q8BYX1 mus musculus
3	619.5	44.7	401	13	Q9PRG7 Q9PRG7 xenopus lae
4	523	37.7	317	13	Q8TFV6 Q8TFV6 brachydanio
5	420	30.3	387	13	Q9PVU4 Q9PVU4 xenopus lae
6	381.5	27.5	235	13	Q8TFV6 Q8TFV6 brachydanio
7	356	25.7	68	6	Q9N139 Q9N139 bos taurus
8	264.5	19.1	143	13	Q919J3 Q919J3 xenopus lae
9	255	18.4	142	13	Q919J2 Q919J2 xenopus lae
10	220	15.9	275	11	Q80WMS Q80WMS mus musculus
11	218	15.7	318	13	Q7T2H3 Q7T2H3 oncorhynch
12	206	14.9	276	13	Q9DDJ2 Q9DDJ2 gallus gall
13	203.5	14.8	483	13	Q800K7 Q800K7 paratichthys
14	201	14.5	289	11	Q8K2X6 Q8K2X6 mus musculus
15	199.5	14.4	267	6	O02764 O02764 cryctolagus
16	198.5	14.3	283	6	Q9XSZ8 Q9XSZ8 cercopithec

17	194.5	14.0	438	13	Q9DFV0 Q9DFV0 brachydanio
18	192.5	13.9	159	11	Q9YKE0 Q9YKE0 rattus norv
19	182.5	13.2	459	11	Q62327 Q62327 mus musculus
20	181.5	13.1	320	12	Q57091 Q57091 ectromelia
21	181.5	13.1	330	12	Q57300 Q57300 ectromelia
22	181.5	13.1	320	12	Q7TDW8 Q7TDW8 ectromelia
23	179	12.9	482	11	Q88734 Q88734 mus musculus
24	178.5	12.9	189	6	Q97530 Q97530 canis fami
25	178.5	12.9	316	12	Q57092 Q57092 ectromelia
26	178	12.8	651	13	Q98SM6 Q98SM6 gallus gall
27	177.5	12.8	446	6	Q95ND3 Q95ND3 felis silve
28	177.5	12.8	1101	5	Q964D2 Q964D2 entamoeba h
29	176.5	12.7	467	13	Q80010 Q80010 gallus gall
30	175.5	12.7	167	12	Q72762 Q72762 cowpox viru
31	175.5	12.7	1074	5	Q964D1 Q964D1 entamoeba h
32	174	12.5	223	4	Q86YK5 Q86YK5 homo sapien
33	173	12.5	305	13	Q800K8 Q800K8 paratichthys
34	171	12.3	285	13	Q9DGH7 Q9DGH7 gallus gall
35	170.5	12.3	167	12	Q9DUL2 Q9DUL2 cowpox viru
36	169	12.2	462	13	Q805B0 Q805B0 gallus gall
37	168.5	12.1	167	12	Q8UYL3 Q8UYL3 vaccinia vi
38	168.5	12.1	186	13	Q7ZZY5 Q7ZZY5 gallus gall
39	168.5	12.1	433	11	Q91ZM6 Q91ZM6 rattus norv
40	168.5	12.1	474	11	Q80WY6 Q80WY6 rattus norv
41	166.5	12.0	189	6	Q95185 Q95185 felis silve
42	166.5	12.0	278	6	Q8SQ34 Q8SQ34 sus scrofa
43	165.5	11.9	320	6	Q9TV79 Q9TV79 cryctolagus
44	165.5	11.9	319	12	Q57079 Q57079 cowpox viru
45	164.5	11.9	263	6	Q9XS60 Q9XS60 cryctolagus

ALIGNMENTS

RESULT 1			
Q8CFT3			
AC Q8CFT3	PRELIMINARY:	PRT:	427 AA.
DT 01-MAR-2003 (TEMBLrel. 23, Created)			
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)			
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)			
DE Similar to nerve growth factor receptor.			
GN NGFR.			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
OX NCBI_TaxID=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Eye;			
RA Strausberg R.;			
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.			
DR EMBL: BC038365; AA038365.1; -.			
DR MGD: MGI:97823; NGF.			
DR GO: GO:0005035; F:death receptor activity; IDA.			
DR GO: GO:0005515; F:protein binding; IPI.			
DR GO: GO:0007411; P:axon guidance; IMP.			
DR GO: GO:0007417; P:central nervous system development; IMP.			
DR GO: GO:0006917; P:induction of apoptosis; IDA.			
DR InterPro: IPR000468; Death.			
DR InterPro: IPR006209; EGF-like.			
DR InterPro: IPR008262; Lipase_AS.			
DR InterPro: IPR001368; TNFR_c6.			
DR Pfam: PF00531; death; 1.			
DR Pfam: PF00020; TNFR_c6; 4.			
DR SMART: SM00005; DEATH; 1.			
DR SMART: SM00208; TNFR; 4.			
DR PROSITE: PSS0017; DEATH_DOMAIN; 1.			
DR PROSITE: PS01186; EGF_2; 1.			
DR PROSITE: PS00120; LIPASE_SER; 1.			
DR PROSITE: PS00652; TNFR_NGFR_1; 3.			
DR PROSITE: PSS0050; TNFR_NGFR_2; 4.			
DR Receptor.			

SQ SEQUENCE 427 AA; 45647 MW; 7AC73263F7E31436 CRC64;

Query Match 93.5%; Score 1297; DB 11; Length 427;
Best Local Similarity 92.9%; Pred. No. 5.1e-116;
Matches 235; Conservative 6; Mismatches 10; Indels 2; Gaps 1;

QY 1 MRAGAAGCAMPRLR--LLILLILGVSSGAKETCTGLYTHSGECKKCNLGEVGAOPC 58
DB 1 MRAGAAGCAMPRLRLLILLILGVSSGAKETCTGLYTHSGECKKCNLGEVGAOPC 60
QY 59 GANQVTCPCCLDNVTSDVYSATPEPCPCTECLGLQSMAPCVCEADDAVCRCAYGYODE 118
DB 61 GANQVTCPCCLDNVTSDVYSATPEPCPCTECLGLQSMAPCVCEADDAVCRCAYGYODE 120
QY 119 ETGHCACGVCVCGSLVFSQCDKONTVCECEPEGTYSDEANHVDPCLPCTVCEPTEROL 178
DB 121 ETGHCACGVCVCGSLVFSQCDKONTVCECEPEGTYSDEANHVDPCLPCTVCEPTEROL 180
QY 179 RECTPWADACEBEIPGRWIPRSTPPEGSSTAPSTOEPEVPEPQDLVPSTVADMTTWG 238
DB 181 RECTPWADACEBEIPGRWIPRSTPPEGSSTAPSTOEPEVPEPQDLVPSTVADMTTWG 240
QY 239 SSQPVYTRGTDN 251
DB 241 SSQPVYTRGTADN 253

RESULT 2

Q8BY1 PRELIMINARY; PRT; 417 AA.

AC Q8BY1
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Tumor necrosis factor receptor 16.
GN NGFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=skin;
RX MEDLINE=22354683; PubMed=1246851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK037248; BAC29775.1; -.
DR MGI; MGI:97323; Ngfr.
DR GO; GO:0005035; P:death receptor activity; IDA.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0007411; P:axon guidance; IMP.
DR GO; GO:0007417; P:central nervous system development; IMP.
DR GO; GO:0006917; P:induction of apoptosis; IDA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR008262; Lipase AS.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PR00531; death_1.
DR Pfam; PR00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH_1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00652; TNFR_NGFR_2; 4.
SQ SEQUENCE 417 AA; 44672 MW; CD0440EF7E70A617 CRC64;

Query Match 89.9%; Score 1247; DB 11; Length 417;
Best Local Similarity 92.6%; Pred. No. 3.1e-111;

Matches 225; Conservative 6; Mismatches 10; Indels 2; Gaps 1;

QY 11 MDRLR--LLILLILGVSSGAKETCTGLYTHSGECKKCNLGEVGAOPCANQVTCPC 68
DB 1 MDRLRLLILLILGVSSGAKETCTGLYTHSGECKKCNLGEVGAOPCANQVTCPC 60
QY 69 LDNVPFSDVYSATPEPCPCTECLGLQSMAPCVCEADDAVCRCAYGYODETGHCAQSV 128
DB 61 LDNVPFSDVYSATPEPCPCTECLGLQSMAPCVCEADDAVCRCAYGYODETGHCAQSV 120
QY 129 CEVSGSLVFSQCDKONTVCECEPEGTYSDEANHVDPCLPCTVCEPTEROLRECTPWADAE 188
DB 121 CEVSGSLVFSQCDKONTVCECEPEGTYSDEANHVDPCLPCTVCEPTEROLRECTPWADAE 180
QY 189 CEELPGRWIPRSTPPEGSSTAPSTOEPEVPEPQDLVPSTVADMTTWGSSQPVYTRGT 248
DB 181 CEELPGRWIPRSTPPEGSSTAPSTOEPEVPEPQDLVPSTVADMTTWGSSQPVYTRGT 240
QY 249 TDN 251
DB 241 ADN 243

RESULT 3

Q9PRG7 PRELIMINARY; PRT; 401 AA.

AC Q9PRG7
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE p75 neurotrophin receptor A-2.
GN PRNTRA.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxId=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hutson L.D., Richards A.P., Bothwell M.;
RT "Life and death in the developing Xenopus retina: The role of the p75
RT neurotrophin receptor.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172400; AAD51031.1; -.
DR EMBL; AF172399; AAD51030.1; -.
DR HSP; P07174; INGR.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR00488; Death.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PR00531; death_1.
DR Pfam; PR00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH_1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00652; TNFR_NGFR_2; 3.
KM Receptor
SQ SEQUENCE 401 AA; 43419 MW; D13BCAF7863BEECF CRC64;

Query Match 44.7%; Score 619.5; DB 13; Length 401;
Best Local Similarity 48.7%; Pred. No. 4.1e-51;
Matches 116; Conservative 32; Mismatches 73; Indels 17; Gaps 5;

QY 18 LLILLIGVSS--GGAKETCTGLYTHSGECKKCNLGEVGAOPCANQVTCPCCLDNVTSS 75
DB 5 LLILLIGVSS--GGAKETCTGLYTHSGECKKCNLGEVGAOPCANQVTCPCCLDNVTSS 64
QY 76 DVVSATPEPCPCTECLGLQSMAPCVCEADDAVCRCAYGYODETGHCAQSVCEVSGSL 135
DB 65 DVVSATPEPCPCTECLGLQSMAPCVCEADDAVCRCAYGYODETGHCAQSVCEVSGSL 124